

Fig. 1A

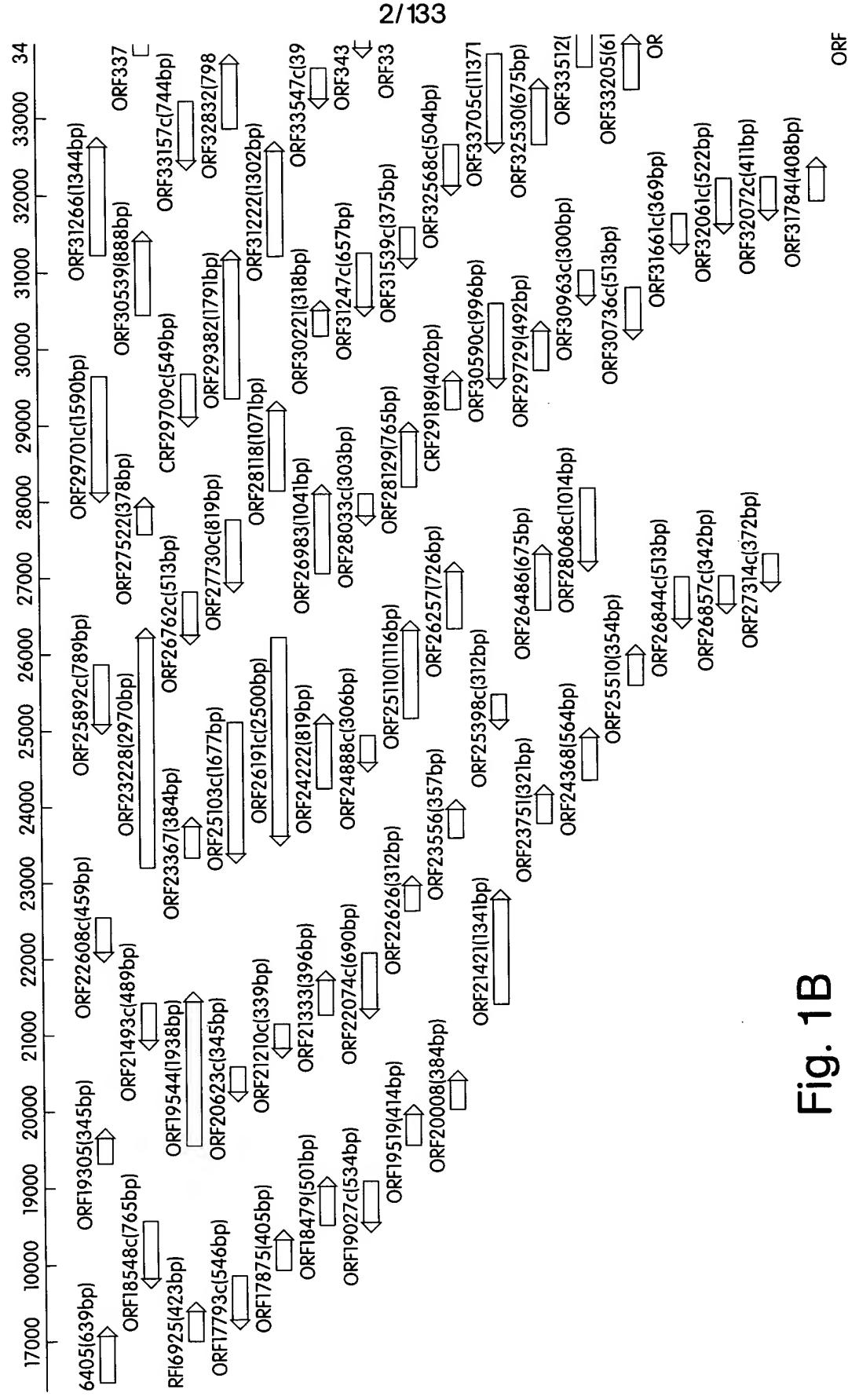


Fig. 1B

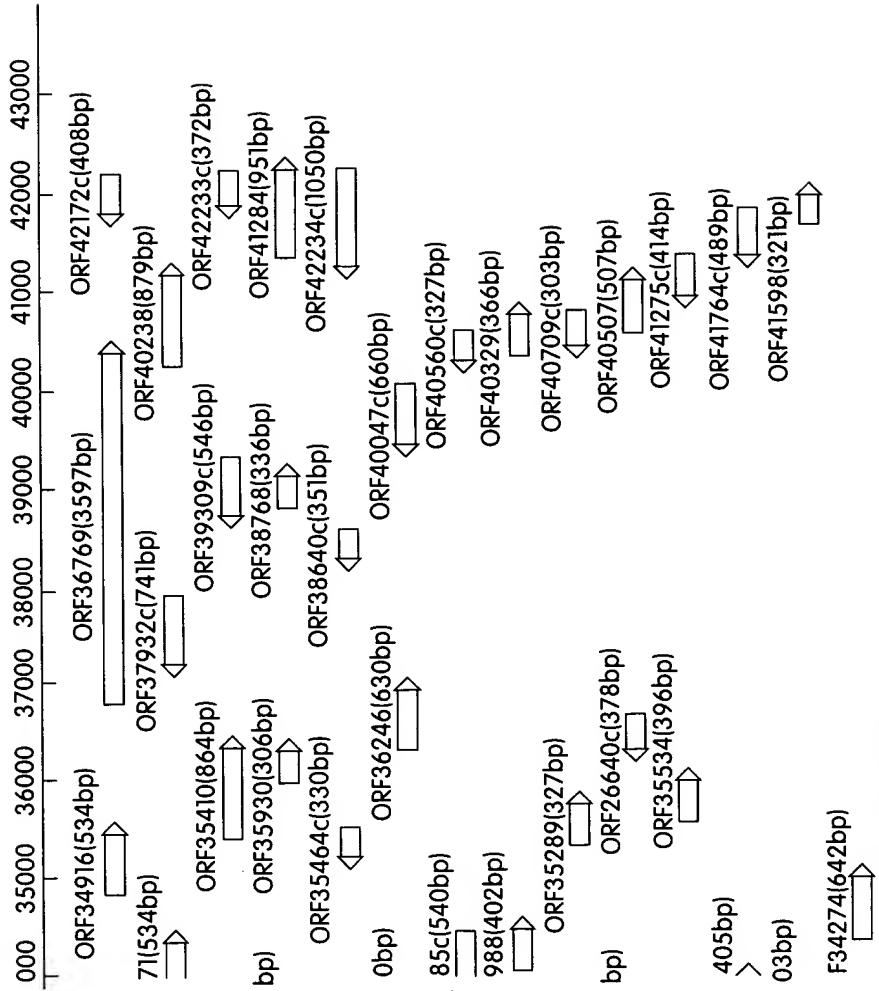


Fig. 1C

34726c(444bp)

B148 SEQ ID NO:1

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 GCGCTGCCCTGGCGGGCTG

Fig. 2A

CTGCTGGCTTGCTGGCTGCATCCGGTAGGGTAGAGCTCTGGTAAGGGCTGCCAGCCAACCACAGCCTTACGG
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Fig. 2B

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Fig. 2D

TCCCTCGTAAGGGTGGCTACGCACCGGGCACCGCTGCGGGATCGGCTGAAGCTAAAAAAATCGCACAAACAGCTTGTAACAC
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 ACCTGACCGTCATTACAGGTACCTGACGAAACATCGCGAACGGGTTCTGGTGCACCAAGACCAAAATAATCTAA
 CGGTATTTGTATCGATGTTACTGCAGGTGATGACTTGCACCGGATTTCAGCACCAAAATTGCTGAATTCTTTG
 GTTCCAAAAAAACGTCGACGGGCTGGATGCGACCCATATAACATGCTTGAGAGGGGGCAAGGATTTGGCTGTA
 TATGTATGCCCAATTGAATCTGAGAGAAAACCTGTCAAATAAGTTTTACATATAGCGCATTGCGAACAGATG
 TTCTAGATTTGTCATGACAATCATTTGCTTAACCTCGTTCGGCGATGGCTAGCGTTTGTGACTGAGGAGG
 CTGCGACTGGTGTCCAGCACACCTGTAATAGACGGCGTACATTATAAGAGAACACCAGGGACTTCGATTAAAT
 TCAGCGTCACCCGACCCATATGGTGGGATTGAGCGAAAACACTTCAATCGCGCGCGCGTGTGGAAAGCGTC
 GATATTTCATGCCACGCTTGATGGGCTTGGTGTGCGATTCTGTGGAGAAAAAAATCACAGAGCCAAGCTCTC
 GCCTTGGTAAGGCAGACATTGTTGGTGTGATGAGGCTTGGTGTGAGCTTCCGTTGGACTATGCCGATTGCGGACCT
 TGCGCAAGCAACCAGCACGCCGCTGAGAGAAAAGACTTCCGTTGGACTATGCCGATTGCGGACCT
 TTGATTTCTCAGCGGCCCTCACACAGAACATCGTACCCCTGATCGTACCCATCGACAAATGCGCACAGGTTTT
 GTCGTTGCCAGAATAGTTACACTCCACCCCTCACCCACGGACAATTGAGGGAAAACCTTCAATTCTCGTCCCCCTG
 CATCAGTGAGTATAAGGCTGCTGGAGTACGATGCCGCTGCAAAATCCGTGTGGGATTTCGTTGACTGCCCTTGATC
 TGTAACACACTCATCAGATTGTCCTCGTCTGGCTGCGAGACGCCACCTGCCATTGTCCTTATACCGGCCG
 ATATCCCCGGATACCGCCCTGAAAGATGACGTCGCAAGGGTGCACCAATCTGAATTTCAAACGCCCTGCTGTGATTGTT
 GGTGAGCGCGAACGTCATCGGCCCTACATAACCTGGAGGCAGCACACTGGAACGTTACCGCCATGGCTGCTGCCAGATAAGTCTGCC
 TGCTTCTCGGAAAAAAAGCGCCGAGATCTCCGAGATCGAATTCTCCATGGTGTGCTGCCAGATAAGTCTGCC
 GGTCCATGACGAAGCAGTCATCCGGTCTGCGAGCACCTGCTGGAGGGTGCCTGAGATTCTCGCAAGCT
 TCCACCCCTACTGTCAGGGAGAGAGGGCTGCGAGTCTGAGGTCAAAATCCAACGCCCTCCGGGGTGGTCAACTCACGGT
 GGGCAAGGGTGTGATAGTTCCATCCGACCAAGTTCAGGAGCGAGTGTGGGAGTAAATCATCTATTGCTCG
 GGAAGGGCTCAGTCATAGCACTGAGCAACCCCTACGTTACAGGAAAAAGTGGACTCAGTGTGCGCGCATT
 TGGCTGTCCTGCCGGTTAGTACGCAAGGACAAAACCGTGCAGACATGCCAGCGCATTTCAGTGCACGGACAGCCCCATC
 GGCATAGCAAGCCTCACGCCACTCTGATTGGCTCACGTCGACAAGAGTCGAGCAGCTTGCAAGGATTTCACATC
 ACCAAAATGCCATGGCAGCTAATGGCGTTCTGCGCTGCCCTTGGCATGACTGGTCAAGTCGGATGCAAACG
 GTGGTCAGCACCAATGCAATTGGGTTGATGCGATGCAATTACGAGTTGAGGCTGGCCAGTTCCTCCAAGC
 GCATAAGAGCCAAGATGGCACATTGCCAACAAATACCCCTCCCCGCTACCGTGTGTTATCGTGTGCGAGCCCTGATC
 TGGCGAAAAGCCGCTCATGATGGCTCCCATGTTCAACTCCTTCTGGATATCCAGGAAGCCGTC
 CCCACCCAAACAACAAAGCTGCCAGGGGATTGATCCTTCTGAGCAGCATGGAACGTCGCGCACGCCCTCGCCG
 CGGGCAGCTACTGGAGAACATCTGGCAGGCCCTCGCTATCCAAGCAGCAATTGAGGAGATCTACCGGCCAGT
 CCAACTATGCCAGCTGGCCAGCAGCTCCCTGCTCGAAAATCATCACCATGCCATCCAGGGGATGATGATCAC
 GGCCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCGATCGCGCAGCGCCGGAGTCAGTC
 AGCCCAGGCTGAAGCCTGGTGGCGCCGCGTATGGGCCCTGGCTCATGACATAGGCAAGATCGTGTGACCTGC
 AGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTGGAACGGACCGATCAACCGCCATACCGCTTCAAGTACGTGAAG
 TCCCGCAATACCGCTCCACGGCCTGCCCTAGCACTTCTCATCCACCAACTGTCACCGCGACTGCACTGACTGATTGGCT
 CAGTCGTTCCAGAGCTGTTGCGTCAATTGATCTACCTGTCGCTGGCAGTACGAGCACGCCGGATCTCGCGAGA

Fig. 2E

TCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTGGCTGCACCGAAGCAG
 TCGCTGCAGCGGCAGTTGGCAGACGGCCTTCGCTCTTGGTAAGGACAAGTCAAGTGAATCACCTAGCGGCCGTC
 TGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTAGCAAGGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTGGCC
 AGGGTATCGATGGGTGCCCTCCTCTAACCGCCGTTCTCAGCATGCTCCAGGACCAAGCCGTACATCCAGACAAATGCC
 GAGGACAAGGCCATTGGACGGCACGGTAGACAACGGTGTGGATGGAGAACAAAGTTCACGCTACTCAAGATTGCTCC
 AGCCTTGATCTGGACAGATGCTGCCAGCGCCCTCACCCATACAGCGGATCACTGGCTGTGAAGATGGAACCGCCCTCAA
 CGGAAAAGCCGAAACGACCTGTGAAATTCCCAACGGGCCGCTGAACAGCAGCAAGCACCAGAACAGAAGATGATGCTC
 CATCAACCTGCGCCAGCGTGTGCAAACCGCAAACGAGACGCAAGCGCAGGCGATTGCGAAACCCCTCAACTGATGATCAAGAAGA
 AACAGACGATTGTATGCACTCTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACGACTGCCGGCTG
 CCTCTCCTACGAACACACGCCGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCTCTGAA
 GCAATTGAAGATGTATTATGCCCTAGCAGAAGTACTGATCTGGACAGGGATTGTTGGTGGATGAAATCTGGCATCGC
 GGCGCGTCCCTGTTCATCAACGACACCAAGGTTGGTCATACCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAA
 TTTTCAAGCGCTATGCCAAGAGCATCCGGTGTGAAAAACTGGCCAAGGCAAGGGAGACGACGGCTGGAAGCTGGTG
 CAGCGCGCTTCGAAAACAGGGGCTCATCGGAAGGACAGTAAAAACCTGAACATCTGGACCATCAAGGTTCTGGTCC
 TCGCAAGACGAAAGAGCTCAAGGCCCTACCTGCTCCAGGATCCAAATTGCTTCCCTGAGCAGCCTCTGGACAACCCAA
 GCCTCACGGTCATCACCGATGCCAAGGAGGTGGAATGACGCCGAGCAGCTCACCGAGGAGTACATCTCGCCACG
 ATCTCCGGAAGCCAGCGCAAGATCTACCGCGCCCGACCAAGGCGCTGCTCAAGCAGCTTCGGCTCTACGCAACCGTA
 CAGGACGTGGACCACCGGGCTGTCTGGATGGCAGCAGCAAGGTACTGGAACAAGGCCGTGCCAAGCGGAGCTGGAACAC
 GTACTCGAATCATCTGGGACGATCTGGGCTATGCCATCGAGCATGAGTTGGTGAACGACTCCAAAGTCAACCCGTTCA
 GAAAGACCAACCGTCACTCCCCCAGCGAGCAAGCAAACCGTCGCCCGAAGCCATCTGCTGCCCGCAATTGGCTC
 AACATGCAGGACGGCGAGCGCTGCACCGCGAACCGCAGCGACCGATCACGCCGCTGGTTCTGGCTTGACGTTGA
 GGTCTTCTACTTCACCGGATCCGGTGAATGCGCTGTTGTCATCCGAAGCGCAGATCGACTGGAAAATCAACTGA
 TCCCATCCCGGGAGACAGAGAGACTCACAAAGAGTTGCTAGTGCCTAAACGGAGGGCTTGCTCACCTATCG
 AGGCTCTGCAAGAGGCCATAGAGCCGATTGCGCTGACGACCAGTTGTCACCGGAAGTGTGGGTGCGGATGACCC
 CGCACCGTTCCGGCACACCTGGCACCGACTTGTGAAGGCACCCGAGCGGAACATTCACCTCAGAAGTGCCTGCTC
 AACCACTCGAATATCCAGACCACGATGAGCTACATCGAGGCCGACTACGATCACATGCGTGCCTGCTGCATGCTAGAAG
 CCTGGCCAAGGCGCGTGGAGAATGTCAGGAAGGTGGATTACAGCGGCTCCCCGCAAGCCTCTGCCAAACCGAAGCCAT
 CGGGCAACCTCTCGCTCGAGTGAAGCGCCGCCACGGAGGCCAGGACAGCGCTGCAGAACCAAGGGAGCACCG
 CCAGGGACAGGCAATTCAAGGAGGTCAACCGCGTGGGAAGCAGATGCGCTACCAACGCCACTGACACCTTCAACCAAG
 CGTGTGTTCACTCTGATGGCTAAAACCTATGCAACCGTGCCTCGGATCCCGCTGCAACAGCGGAT
 CAGGCGGATGGGATCTGCCGCCGAAGCAATCTGCTAGCGATACCGTACTGAGGGCCGCTACCGACGAAAGGTA
 GCCGTGCCCTCCAGCAGATCGTTAGGCTGTAGGAAAATCTGGAATTACCGAGAGCGCTGGATTCCAGGCCGGCATG
 CTGGCAGAGCCAGCGCAATTCAAGGCCAATACCAAGTACCCCTGTAATCGCTGATTACGTCGGGGCGCATGCTAC
 GCCTGCAGAATGGTTCAAGGGCTTAGAAACAGAAAAGCCACCTAGAAAGGCGGGCTATTCCATATTGACATCACGTCA
 ATGCGGGCTAAATGTTGCCAGACGGCTGCTAGACAAGAACCGCGTAACACCCCTCTAGCCTATGCAACTCGCC
 CGTAGAAAATGGTGGTGTAGGATTGCAACCTACGACAATTGGTAAAGCAGACTGCTCACCGACTGAGCTAAC
 GACCCAAAGTATGAGGTTGGTAGAGAGATTCGAACTCCGACATCCTGCTCCAAAGCAGGCGCTACCGACTG
 CGCTATACCCGATTGAAATTGGCTCCGCGACCTGGACTCGAACCCAGGGACCAATGATTAACAGTCAATTGCTCTACC
 GACTGAGCTATCGCGGAACGTCTTCTTCAACCCCTGGACGCTTCCGGTGTGCTGGATTGCGCTCAGAGGCGCGCCA
 TTTTACGGATGCGCGCGGGCATGTCACCCCTGATCCAAAAGTTTCTTCTTCCACGAGCGACAAACGGCCCT
 TCCACTGCATGCGGAGCGCTCTCGCGCTACCGACGCCATGAAAAGCCCCGCCAGCGGGCTTCCCTGCGC
 CCCCGAAGAGGTAGCGCAAGACGATCTCGTCCCTCCACCTCGCCAGATACTGGCACCCGGCGAATTGCGGCC
 CAGGATCAAGTGCGCCAGCGGGTTCTCGATCCAGCGCTGGATGGCCCTTCAGCGGGCGTGCCTAGACCCGGCTG
 AGCCGACGGCAATCAGTTGTCCAGCGCCTCTGGCTCAGTTCCAGGCTCAGCTCGCCTGCCAGGCGCTGGCAGG
 CGACCGAGCTGGATCTGGCAGTGCCTGGCATCTGCTCGCAGCGCAGCGGCTCGAACACCACCTCGTCACTCCGGTT

Fig. 2F

GATGAATTCCGGACGGAAGTGCGCATTGACCGCGTCCATCACTGCGGCACGGTGCCTCGGGTCGCCGCCAGCTCT
GGATCTGCGCCGAACCGAGGGTGGAGGTATCACCACCGTGTGGAGAATGTTGAATACATCCGGATGGGCTTCTCCACCTCGTCCAGCAGCAC
AGGCGTCCGTCTCGAGCACCTGGAGGAATGTTGAATACATCCGGATGGGCTTCTCCACCTCGTCCAGCAGCAC
CGAGTAGGGCTTGCAGCGGATGCCCGTCAAGTAGGCCCTTCCCTCGAAGCGACGTAGCCGGAGGAGGCGCGGATCA
GGCGGGCACCAGAGTGGCTTCTCATGAACTCGGACATATCTATCCGACCCAGCGCTCTCGGTATCGAAGAGGAAC
GCCAGCGCTTGCACAACTCGGCTTGCACCCGGTGGGGCGAGGAAGAGGAACGAGCCGCTGGCCGGTTCGGATC
GGCGAGGGCGGGCGCGAACGGCGCACGGCGTGGACACGGCAGTACCGCCTCGTCTGGCGATCACTCGCCGATGCA
GCTCCTGCTCCATGCGCAGCAGCTCTCGCCTCGGCCCTCGAGCATCTCGACACCGGATACCGGTCCACTTGGAAAC
ACTTCGGCGATTCCCTCGTCGGTACCTTGGTGTGCGCAGCAACTGGTCTCGGTCTGCCGTGCTGGTCGACCATCTGCAG
GCTCGTCCAGGTCCGGGATGGTCTGGTACTGGATGCGGCCATGCTCTCGAGGTGCGCCCTTGCGCCGCGCCCTCCA
TCTCCTGCTTGGCCTGCTGATCTCTGCTGGATCTGCCGAGGCCCTGCACCTCGGCCCTCTGGACTTCCAGATCTCC
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TTCCCTCTCAGCGCCTCGCGCTCGATCTCAGCTGGATCAGGCGACGGTCGAGACGATCCAGTTCTCCGGCTTGGAGT
CGATCTCATGCGGATGCGGCTGGCGCTCGTCAAGTCAGGCGATGGCCCTTGTCCGGCAGTGGCCGATCGTGTAG
CGGTGCGACAGCTTGGCCGGCGATGATCGGCCGTCGGTGTGCTCACCCCGTGGTGCACCTCATAGCGTCTTGGAG
GCCACGGAGGATGGCGATGGTGTCTCCTCGCTCGGTTCTGGACCCAGCACCTCTGGAAAGGGCGCTCAGCGCGGCA
CTTCTCGATGTACTGGCGATACTCGTCAGGGTAGTAGCACCGACCGAGTCAGCTCGCCGCGCCAGAGCGGGCTT
AGCATGTTGCCGGCGTCCATGGCACCTTCCGCTTGCCTGGCGCCGACCATGGTGTGCAAGTTCGTCGATGAAACAGGATGAC
CCGGCCTCCCTGCTTGCCTGCCAGTTCGTTGAGGACCGCCTCAGGCGTTCTCGAACTCGCCGCGGAACTTGGCACCGGGCGA
TCAGCGCCCCCATGTCAGGGCCAGCAGGCCCTGCTTGGCCGACTTCGCGCTTGTGATGATGCGCTGGCC
AGGCCCTCGACGATGGGGCTTGCCTGGGCGGTTCCGCGACCGATCACGGGTCGAGCTTGCCTTCCCTCGCGCGCTTGGTCA
CTGGATGGTCCGGCGGATCTCGTCGCGACCGATCACGGGTCGAGCTTGCCTTCCCTCGCGCGCTTGGTCA
CGGTGTACTTGTCCAGCGCTGGCGACTCTCGACGGTCTGGGTGTTCACCGCTTCCGCGCACGAGGTTGGCCACG
GCATTCTCAGCGCTTGCAGCACGCCCTGGCGAGCAGCAGTTGCCAGGCTGGTGTCTCGTCCATCGGGCCAG
CAATACCAGCTGCTGGAGATGAACTGGTGCCTCTGCTGGGCCAGGGCGTACGCCCTGGTGGAGCAGCGTGCAG
CTGGGACAGGTTACGTCGCCGGTGGCTCTGGATCTTCCGGCAGCGCGTCAAGTCTTGTGAGGCGCTGCGCAGG
GCCGGCATATCGAACCGACCTGCATCAGCAGGGCTTGTGATCGAACCGCTTGTGCTGAGCAGGGCGAAAGCAGGT
CACCGGCTCGATGGCCGGATGGTATGGCATGGCAACGCCAGGGACTGGCGCTGGAGAGCGCCAGTGCAGCTGCTGGTCA
AACGGTCTATTGCGATGGTCTGCTTCTCTATAGAGCGGGCCGGAACGATGGGTGTCCTGTGATGAAAGAAAAGCCCG
CGAGATGACTCAGTAGATAAGGGCATTTCGCGGTTCAAGCGACCGGACCGTACCGTCAAGTGGCCGAGGCGGGATAA
CTTGCCTGGGGCTAGTCCCTGGAGGCCAGACCAGGCTGGCAAAACGGCCGGTACCGCAGGCGGGCGTAGGAATAGAAGCG
CGCGGTATCGCTGAAGGTGCGAGAGCGCCGATGCAAGCGGGCTGACGCCATGGCGCCAGGCGGATCCGCGCAG
GGTAGATGCGCCATGAAGCGCCGGATTGGCGCTAGGTACGAAAGCGAGCGCCTCGCGCTGCGCAGCGACGAAT
GCATCGGGACCTCGCCGCCGACCTCGAAGGCCCTGCCGGGATCGCCGGCCAGCCAGACCAGCAGTTCGTCGCCGG
CACGCCAGGCTGTCACCGTCCGCCAGCAGGCCGCCAGCCGCCAGCCGGATGGCGCCAGGCCACCGGGGG
TGCCCGAGCGGTGCGAGAACACGCCGGCAGGCGAGTCGGCGGTGATCGTACAGGCAGGCCGGCATCGCGCTCCAG
CTGGCGTCCGGGCTGAGCACCGGTTGGGTGCGCTCCACCGTCACTCCGTGCACTTCCACCGTCA
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CGCGGATTCCTCATGCGCACGCCGGTGGCGGGTATCCAGTTCGAGGAAGCGCGGTGCGCAGGCCCTGCCGGGG
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AGGGGATAGCCAATATGGCTCATGTGACCGGGATCTGGTGGTACGCCGGTCTCCAGCTGACCCGGTACGCCAG
CGCACGGAAGCGTTCCAGCACGCCGAATGGCTGACGCCACCTGCCGGTACGCCAGGCCACGCCATCTTCTGCCGCTGCA
CGCCATGCCGTCCGATGCCGACCGATGGTGCCTGGCGGGAGGTGATCACGCCGATCACGATGCCCTCGTAGATGCCGCTG
ACCGACCGTGCCTGCAAGTGCAGGCCACAGCTGGTGTGGCTCCAGCGTCTGGCCACTACCATCAGGCCGGTGTGTC
CTTGTCCAGCGGTGGACGATCCCGCGCGGGCACATTGGCGATGTCGGGACATGGTAGAGCAAGGCATTCA
TGCGTCTGATGGCCGGCAGGCCGGATGGACCAACCAGGCCGGTGTCAATCACCAGGATGTGCTCGTCTCGTAG
ACGATTTCCAGCTGATGTCCTGTCGAGGCCACTGCCCTGGCTTCTGCTGCCCTCCAGGCCAGTGTGCGGCCGCT

Fig. 2G

Fig. 2H

AGCAGGGCCTGTTCCAGGCCAGCGGTGGCACCTGTTCTCGACGAAGTCGCCGACCTGCCATGCCATGCAGGTC
 AAAC TGCTCCGGCGATCCAGGAAAGGCCGTGCGCGCGTCGGCGGCCAGCAGGAGGTGCCACGTGCGCATCC
 TCTCGCCACCCACAAGGACCTCGCCGCGAAGTCGGCGCCGGCGCTTCCGCCAGGACCTACTACCGCCTCAACGTC
 ATCGAGCTGCGGTACACCGCTGCGGAACGCCGAGGACATCCCGCTGCTGCCGAACGCATCCTCAAGCGCTGGCC
 GGCACACCGCCTGCCGCCAGGCTGACCGCGACGCCAGGAGAAGCTGAAGAACTACCGCTCCCGGGCAACGT
 CGCGAGCTGAAAACATGCTGGAGGCCCTATACCCCTGCGAAGACGACAGATCCAGCCTCACGACCTGCGCTGG
 CCGATGCGCCGGGTGCCAGGAAGGCCGCCAGGCTGAGCGAAATCGACAACTCGAGGACTACCTGAAAGACATC
 GAGCGCAAGCTGATCATGCGAGGACTCGAGGAGACCCGCTGGAACCGCAGGCCGCCAGGCCCTGGCCTGACGTT
 CCGCTCGATGCGTACCGCCTGAAAAAGCTGGGATCGACTGAAAGTAAAAGGCTGTCCGAAGACAGGCCCTTGGTT
 TTCGCTCTCAGAGGGCAGCAGCGGGCGTAGGGGCCGGTCGATGATCGGTTCCGCCGCTCATGAGATCCGCCAG
 CAGACGGCACGACGCCGGTCCAGGACCCAGGCCGTTGCGTAGGCCGGTATTCAAGCCAGAGGCCGTCGAAGGCCAGGCA
 CCGGACCGATATAGGGATGCCCTCGGGAGAGGCCGGCAACCCCTGCCAGGCTGAGGCCACCGGCTGATGCGCCAGT
 TCCGGCAACAGTTCTGCCAGACGCCCTGAGGCTTCCAGGCCCTCGCGTGGCTTGTCAAGCCGAAATGTC
 CAAGGTGCTGCCGATCAGGATGTGCCGTCGCCGCGGAATCGCTAGGCCCCCTGGCCAGCACCATGCCGCCAGGA
 AATCCGCCGCACTTGTAGAGGATCATCTGACCTTCAACGGTACCAACGGCAGTCCAGGCAAGGCCCTCAACAAC
 TCGCCGCTCCAGGCCCTGCCGCCAGCAGCACCTGTCGCCACGGATCTGCCACGCCAGGTCGCCACGCCGACACTCG
 ATCGCCGCTGCCAACAGCCGCAACCTCCGCTGTTCATGCAACTCGAGATTGGCAATTGTTGCAAGGGATGCCGCA
 ATGAGCGGCCAGGCAGGATTGCGCACATTGCCACGCCGACATGTAGACGCCGCTGGAGGCCCTGCCAGGCC
 GGCACCGCCGCTAGGCCCTCGATGCCACTTCCCAACGCCGGGTGTGGTTGCGTAGGCCACTGCACTGCCCGT
 CTGGTCTCCAGGTCCAGGCACTGAGGCTACAGGCTATGGCTAGGCTCGAGGCCGGTCTGGTCTGAGCAAACGCTGCC
 CCAGGGCCGGTAGAAGTCTGCCAGGCTGCGACAGTGCAGGCCAGGCCCTCCACCAAGGGTCAACGCCAGTCCGGCAGGCC
 ACGATCCCGCTCCGCCAGGATGCCCTCACGCCACTCTGCCCGCTCCACCAAGGGTCAACGCCAGTCCGGCAGGCC
 CAGCTCCGGGCGGTCAACAGGCCAGTGCAGGCCAGGCCCTACCAACTACATCTACTCACCACAGGCCCTTACCGA
 TTTGCCAGGAACAGAGAAATACTCAAAGGATCAGATGCTGACGAAATTGCTGCTCAACGAACTCAGTCGAATCTA
 GTCCCGGTAAAAGCCATCATAACCGCAGAGGATTCAACGCCAGGATGAGGTTGAATTGGTGAATTGGTGAACATCGA
 TAGTCCTATCGATCCTGCCAGGCTGACATTGCGCTGCCACCCCTCCCGACAGAATGAGCGGGACATTAGCCGT
 GATATTGGTGAAGCCTGACTAGTCATGTCAGGCTGCCGGCTAGCAGCATAACAGAACGGCTGATCATGAGGTGTG
 CGGTAGCGGTGACGGCAGTACCTGCGAGGAAATGGCATCTCGGCTGGTTAGCCGTAACGACAGGAGCAACAGATA
 TGGCCCGGCTGAAATACGAGTCGACCGATATTCAACGCCGGGCTTCGACAAGCGACTGCCCTACGCCCTAATGGC
 ACCAGCCCTACAGGTAAACGGCGTTCTGAAATGTAAGGACGATGCCATCGAGTGGCAATTGGTCTCAATGCCAAGG
 CCGCCTCAGGGTGGCGGGAAAGAGCGAAATAAAAGCTCTTACCTGTGCTCCAGGCCGGTGGAGAGAACTGTTACAT
 ACCGTTGCCAGTCATCCACTCTCCGCTCCGCTGTCTGCTACAGGGACAATGCCCTCCACTAGGAAGATTATC
 TGGCCCTTCCCTGTTGAGTACTGCATGCCCTATTGTCGCAAGGCCGGTTTCCCTGATCGAGTTGATGATGGT
 TTGGTCTGGTGCCTATTGCCAGCATGCCGTACCCAGTTCAACGCCCTGATCGAGCGAACCGAATCCAGACTGC
 CAGCGAGGAACCTACGCCCTGCTCAGTACGCTCGCAGCGAAGCTGTAACCGCTCATGCCAATGAGCATCGGCC
 CGCAGAACATGACTGGCAAAAGGCCGAAATCATCGCCGCGACCCAGCTGCAAAGCACCAAGGTTCCAGCAG
 GTCTCGCTATGCCAGCAGTGCAGTGCAGGCCGGTACCTCAACGCTACCGCACACTTAGCAACCCAGGCTGCAAACAT
 TGACATAAAAGGCTGCTTCCGGGTGACAAAAGTACAGGACGCTGCTTACCGCTGAGGCCAGTGGACGCCGATCTGT
 ACCCATCTCAAAGCAACGGACAGCTGAACTGAGGAAAGCCATGCTCGAGAAAAGGGTTTACGATGATCGAAGTA
 CTGGTTGCTCTGGTGTGATCAGCATTGGCTACTGGCATGGTCCATGCAAGGGCGCACGATCCAGTACACGCCAGGA
 GTCGGTACAACGCAATGCCAGCAATGCTGCTAGCGACCTGATGGAAATAATGCGTGCAGGCCAGATGCCGACTCTA
 ATCTACGCCCAACTACGCAAGACTGCCCTACTACAAGGCCAAGGGCAGCGACTTCCCGCAGGCCAGCGCTGC
 GCGCCATTGCCAGCAGATGCTAAGGAACGCTCGGCTGCTGGGCCAACAGGCCCTGCAAAGACTTGGCCGGAGGCC
 ACTCTTGAAATGCCAATTCTACATTGTCGCAAGGCCAACCCGGTACCTGCGACAACACCAAGGCTGCCATGAAA
 TCCAGGTTGCTGGCGAGCCATGGATGGAGCGTGTTCAGCAACGCCCTGACTCCACCTTGTCGACCTACAGCGTCC
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 AGCAGCTTCTGATCTGGGATGCCAGATCTACATCGACAACAAACGCAACTATCTTCCAGCAAGGCCAGGCC
 CAACCAAGGAAAATAGCCGCTTGTCTTATGCTGCTGCAAGCAACAACTGGATAAGACAGCCATCGTCGCC
 ACAACATGGAGAACATGCTTCAAATCCGCAATTCAATGGCTGCTGCAATTGTTGCGAGACTATCGCTGCC
 ACTGCCCTCAAGGCCGGTGAAGTACGGTGTGCTTGCCTATCAACCCGCCAACAGGGGAGCATGATTGCC
 CGTAA

Fig. 21

TGAAATTACCGGAGTTCGGAAAAGCCCTTACAAATACTCCCCGTGTCGTCGCTGGCTACCTACCGAGCGCCG
 GTACCCCTGAGTTGCACTCGTCCCGATATCGCCAGTCGAATCGGAGAATTGGTCAGTGGCTCACAGACTCCGCTT
 GAAGCGGGGGTCGGGCAGCAGATCGTAGCGAACGCAAAGTATCCAGCTCGTCGCACTACAGGATGTCGCGGTGTC
 TATCCGAGCATTGCGCTTCTCAATCTGGCAGGCAGCGACAATAACAGCCTGCGCACAGGAGATGATAGCCAGGCACGCG
 ATCGCTGGATCGCTTTATCCGAGAGCAGAAAGCGCATCGAGGCCAGACAAAGGCCAGATTACCAAATAGCGCT
 GGTAACCAAACCATCGGAATCTCATGCCATGACCCCTGCCATACCTCTCGACAGCAGGGATCCACGTTGTTGATCTCG
 CTGGTTATCTGTTGATGATCACGCTCTCGCCGTTCCAACATGCGGAGGTGTCAGTGGAAAGCCGTATCACGGCAA
 TCTCATCGAACAGAAGCGCTGCGAATGCGGGGAAGCTGGCTACCGGAAGGTGAAACGACGCTTTCAATACCATCA
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 TCTGACAGTTATGCCGCCACGGCCCTGAATGTCAGGCCAGCAACCCCTGTTCTAACCCAGGGGTTGCTCCAAACCTGCT
 GTTCACTCTAGATGACTCAGGCAGTATGCCCTGGGCTTACGTGCCGAGCGTATTAGCGGGAAATAGCGGCAGAGCGGGAC
 GTTCCAGCAGTACAACGCACTGTAATCAACCCCGATTATGCTTACCAAGTGCCAAGAAATTGACACTGTCAGGCGAT
 CAGATCATCGTTCCGACTATCCAGTGCACGCTCACAGCAGCCTGCCAGGATGGCTACGCCAAGGCTCCACCAACCAA
 CCTGAGCAATAACTATGCCCTCAATGGGAAACGGCTGCCGTTGCTGATCGATAGCAGCTGCAATACCGGGAGAGCTT
 ATTACTATACTTAAAGGTAAGCGTAGCTGCCCTGCACAGCGGTGAGCAGCTCAACTCCGTTATACCTACAATGCT
 CTTCTACCAAGTCAGGAAAGCAACTTGCATGCGTACTCCACTATCGCAACCGCATCTGCCAACAGGCTCCACCA
 CAACCTGGCTTTACAGCCTGCCGAAACGCTGCGTCTCACTGGGGGCCCTGAACACCTGAGCATCGGCCAACACA
 GCAGAAGCTGCCAAACAAATGCCCTGCTCCAATTCAACAAGCAGCACAAATCAATTCTCAATTGGCTGCCAACAGC
 CGGCCAGCGCGGTACTCCTCTGCATGCCGCTTGCACGCCAGCGCTTGTCAAACCAACGGCACAGCTTATAC
 CACCGAAGACGGAAAGACATATTCTGCCGGCCAGCTATCACATCATGATGCCAGGTTATCTGGAACGGTCCGAAC
 TCACCCCCGGCAATCTGACAACCAAGAACAGACCTTCTGATAGCACCCCTATAGGCCACAGCCCCCTATGCCGAC
 AGCAATGCCAGCTATGGCTGACCTGGCTTCAAATACTGGACCAACAGACTTACGCTCCAGCATGACAATGACCTGAA
 GCCTTCATGCCCTACAAGAGTGGGACGATCCAAGGATTACTGGGACCCCTGCCAACACCCAGCCACTGGCAACACA
 TGGTCAACTTACGCTGGCTGGCCTAGGTCTTCCTATTGCTCACATTGAACTCTGCAACCAACTGGACAGGCAACCTT
 GGCAACTACGAGGAGTTGATGGCTGGAAAGCAAGGCTGGCCAGCGTCGATAACGACGCCGACCCGTAACGCTACGA
 CCTCTGGCATGCAGCTATCAACTCTGTTGGAGACTTCTTCTGCGGAAATCAGCGACTCTCTGGTCAGGTTCAATA
 AGATCCTGACACGGATTCCGAGCGAACACCTCTCCAAACAGCAATGACTTCCGCGCTGCAGGATGACGGAAACC
 GGCAGCAAGCTGATCCGCTACAGCTACCGAGCTTGCAGTGAAGAACTGGGGGGGACCTTATACGTTACAA
 GGTGGAGTCGACTTCAACGGGCTGACCAAAACCCAGGAATGGAGCGCCGCGACTGCTGGCAACCGAGCTCCGCTA
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 TTAGCCACTGGCTGACCGAACCGGACAAGGACAATCAGGCCAACCAAAGGAGCACAGGGGGTCGACTCATCCG
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 CAGCGCAGCCCTAGAGTTATGTTGGATCCAACGATGGCATGTTGATGGTTCAACATCAAACCGGCGTGGAAAGAGTT
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 GGAGGTGCGGGCTGTCGACTCGATGTAACCAAGCCGACGATGTCAGCTGCTTGGGAAATCGATAGCAGTACCGA
 CTCGGACCTGGTACACCTCTCCAAACCTACCGTAGCCAGACTGCACAGCGGACAATGGGAGTAGTTACCGGCAACG
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 CTATGCTGGCGATCTGCAAGGGAAATATCTGGCGCTTGCATTGATGCCAATACCGCAACGACGACCCAGACACAAATA
 CCTCTATCAATCCCTCAAGCCCCGAGATGTAAGATCCCTGCTTCAAGAGTATCGTTAGCGGCCGCCCCGTTTCCG

Fig. 2J

GCTCGCGCCGACAACAATCTCGTCAGCCCCATCACGGCTCCGCCTACCTTGGTACGCCATCCTAGCCGTAGGGCTACAT
 CGTCATCGTAGGTACAGGAAAATCTCGAGGACATGACGCTCAGGGCATAACAGCAGCCGAGGCATGACGCTCTATGGTA
 TCTGGGATCGCCAGACCAAGGGCGAAAGCGAAACAGTACCCAAACCATCGACCGCAACGCCCTCACAGCCAAACCATG
 ACAACAGAGGCAGACTCCACATTGGTAGCGTAAACAGGAATATTGGCTTATTAGCCAAAACCGGTGAAGTGGTACAA
 AGACGGAGCAACCGTACCGGAACCTGGATGTGGTAGCTATGGCTGGCAGCTGAATCTGGAGGTCAATAGCAGCAAGA
 AAGCGAAATGATGATCGAAGATATGTTGCTGCCGCGCAAGTGTCTTCTATTGCAACGCTTGACACCGAACGACGACCC
 TGTGACAGCGCTCTACCAAGCTGGACCTACGGCTCAATCCATATACTGGCGGACGTACAGTTCACCGTCTCGATCT
 CAAACGTGCGGGTATACTGGACTCTGGCTCGGATTACAACGGCTCGTGTACCGCTTCCAAACAGGATGGACTAGGTG
 GCTTGGCATTACCCAGAACGAAACAGCTCAATCCGAGGCTTGCACTGGTAGTGAAGTGCATCATCTCAACCCAGCGAC
 AAGAGTAACCGGACGACAAACCTGGCGGTGTCGAGGAGAAATGAACATGAACCCCTTACGTCTTCTCGCACAGCTCT
 GCAGCTCTAGCTCTGGCTGCCAACCTTGCGCTTGAGTGCACGAATACGTTGAGAATGTGGCGTGGTAGGATGT
 TCATCCTGCCGCCGGTCTGGTAGTAGTCGATGGGAGACATATCGCTGCCAACCGTGTCCAACAAACAGGACTGCCGG
 TCATATTCTGGTACGTCAAGGACAGACAGTGTCTTCTCGGCAAACCTCACCAGCGACCTGCCAGAAATCGAGTCGTT
 TACATTATCAAGCAGGCCCTCTCGTCTCGGATCGAGCAGCAACATGAAGTCGAACAGAGGCTTCACTCTCATC
 GAGTTGATGATCGTAGTAATCATCGTATTCTTGCTGGTAGCCTACGACAATACGTAAGCAGCG
 GAATCGCACCGAAGGACAGGCATTACTCAGCGAACGAGCGCTACTCAAGAGCGCTATTTTACAGAACAAACTTATA
 TCACTACCCAAGCCGACATCGGCAAGCTGCATATCGCAACACATCGGCAACAGTGAAGTCTCCACAGGCAAATAC
 AGCCTTACCGTCGATACGGTAGCCAACGACGGAGGTTATCGCCTTATCGTAACCGGATTCAACGATCTGATTGTGG
 CAACCTGACCTTGACGCCAACGGCGAGAAAGGCCGACTGGAAGCAAGAACAGGCTTGAGAATGCTGGCGCTAAAGCG
 CCGAGACAAGAAAAGCAAAGCCGGCATAAGCCGGCTTTTCAGTGCACAAATTCCGATTACAAGCCTTGACC
 CGCAGTTCTGGGATCGAGAAGGTAATGTTCTCCCTCCAGTCCCTGCTCTCCGACGCCCAACTCACG
 TAGCTGGCGATCACTCCGCGCACCGACTCCGGCGGGAGGCGCTCGGTGATTCCGATGCGACGCAACCGTGA
 ACCAGCCGCGTTGCATGTCCTCGGCCGTCGATCAGTAGGCCGGCGTCCGCGAGTTCCGAGGCG
 TTGGAGTTGAACTGTTGGGGCTGCCACCACAGGACCATGTCGACTGGCGCCAGTCCCTCACGGATCCTGGCG
 GTTCTGGGGCATAGCAGATGTCGTTCTGGTCACGTAGTGCAGGGCTTGGCGCACCTCCAGCGCGGACG
 TCGAGGTGTCGTCATCGACAGGGTGGTCTGGTCACGTAGTGCAGGGCTTGGCGCACCTCCAGCGCGGACG
 TCGGCCTCGTCTCCACCAGGTAGATGGCACCGCGTTGCTGGCATCGTACTGGCCATGGCCTTCCACCTCGGGTG
 GCCTCATGCCGATCAGCACGCTTCGTCGGCGCTGCGCGCTGTAGCGCACCACTCCATGTGCACCTGGTACCGAGCG
 GGCAGGTGCGTCGAAACCTTCAGGCCGCCCTCGCTTCCGCGACCGCCCTGGGAAACGCCGTGGCGCTGAAG
 ATGACGATGACGTTGTCGGCACCTGATCGAGTTCTCGACGAAGATGGCGCCGCTGGCGAGGTTGTCACGACGAA
 CTTGTTGTCACCACCTCGTAGCAGTACGGCGGGCGAAGACATCGAGGGCACGGTTGACGATCTCGATGGCG
 GATCCACGCCGGCGAGAACGCCGGGGATTGGCGAGTTGATTTGATGGCAGGCCGCTCGTGGCGACGCCGTGATTGGAC
 GAATGAACCTTGCTACCGCCCTCCCCGTTGGGAAGGGCGAGCGACCGACGGTCAAGCCGCTGGACGTCAT

Fig. 2K

>ORF2 (SEQ ID NO:2)

TCGGCGATCCAATGCCAAGGAGTACCTGGGCAATCAGAGCCTACTCACGGCTGCCGGGCCGCATTGCCAAGCTCCTGG
 ACGCCGACGAGAACAAACACCAGTACCGTCTTCAGCGAACGGCACCGAGCTCGGGACGACCGGAACCAACAGCAACTCG
 GCCCTCAACAGCATCCTCTCCGGCGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACGGGGAGGCCCTCGCCGC
 CGTCTACGTGCAGCCAGGTGCGCGGGTGCAGTCATCTCGATCAGCAACTGGCGATCGACTATGA

>ORF3 (SEQ ID NO:4)

CGCCGATCCAATGCCAAGGAGTACCTGGGCAATCAGAGCCTACTCACGGCTGCCGGGCCGCATTGCCAAGCTCCTGG
 CGCCGACGAGAACAAACACCAGTACCGTCTTCAGCGAACGGCACCGAGCTCGGGACGACCGGAACCAACAGCAACTCG
 CCCTCAACAGCATCCTCTCCGGCGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACGGGGAGGCCCTCGCCGC
 GTCTACGTGCAGCCAGGTGCGCGGGTGCAGTCATCTCGATCAGCAACTGGCGATCGACTATGAACCAAGGGCCGAA
 GGTCGATTACAGCTCTGGAGGCCGCTATGCAACAGCAGACTTGGACTAA

>ORF602c (SEQ ID NO:6)

TCGGCCTGGTCAATTGGCGAGGCATCCTGCTCGGATCGATTGGGCGCCGCAGCGTTTGCCTGGCATCGAGGAGCAGCCG
 GCCACGGCTGTTGCCTATCGAGCTGGTCGACCTCGCTCCAGACGTCGAGCATGTTGGCCTGCCGTGGGGCAGCATCT
 CCTCCTTGTGGTGGAGCACGCTGCCAGGGTCAGCGCGCAGGCCAGGCCGGCGCAGAGACGAAGAAGGGGGTAGTC
 GTCTGCTGTTGCATGAGCGGCTCCAGAGCTGAATGACCTTGCAGGCCCTGAGTTCATAGTCGATGCCAGTTGCTGAT
 CGAGATGCACTGCGACCCGCGCACCTGGCTGACGTAGACGGCGGCGAAGGCCTCCCGTACAACATTGTCATCCACTGC
 CGGATGTGCTGACGCGCCGGAGAGGATGCTGTTGAGGGCCGAGTTGCTGTTGGTCCGGTGTCCCAGCTGGTGC
 GTTGCCGCTGAAGACGGTACTGGTGTGTTCTCGTCGGCGTCCAGGAGCTGGCAATGCCGGCCCCGGCAGCCGTGAGTA
 G

>ORF214 (SEQ ID NO:8)

ACAAGTTGTACGGGGAGGCCCTCGCCCGTCTACGTGCAGCCAGGTGCGGGTGCAGTCATCTCGATCAGCAACTG
 GCGATGCACTATGAACTCAAGGGCCGCAAGGTCGATTACAGCTCTGGAGCCGCTATGCAACAGCAGACTTGGACTAAC
 CCCCTCTCGTCTCTGGCGCCGGCTGGCTGCCGCTGACCCCTGGCAGCGTGTCCACCAGCAAGGAGGAGATGCTGCC
 CACGGCGAGGCCAACATGCTCGACGTCTGGAGCGAGGTGCGACCGAGCTCGATAGGCAACAGCGTGGCCGGCTGCTC
 CGATGCCAGGCAAACGCTGCCGCCCCATCGATCCGACAGGATGCTCCGCAATGACCGAGGCGACTACACCCGCA
 CGGCCAGCAACGAGATCCACAGTCAGTTCAAACGACTGCCAATCCGACCTGGTGTATGTGTTCCCGCACCTGCC
 GGCAGCGATCCCGCCCCGGTACCGGGTACACCACCGTGTCCCTCTACCAGCGAGTCCAGTCGCCATGCCGGCGA
 ACGCACGGAGGACTATTGA

>ORF1242c (SEQ ID NO:10)

TCTCGTCTGGCGTAGAAACTGGACAATCCAGGGTGAGGTTCTGCTCGTCAAGGAGTTCTGCAGGGCTCTTCAAT
 GCGTCCCGGGCGTTCTGCATCCAATTGGGATCGCGCCCTCGGTGCCAAGGGCACAGCTCGAAGAATCGGGCGCGCA
 ACGCCCATTCCAGGAGCATCACTGCTCGGGCAGGTACTCACGCCAGGGCAGCAGGTCTACGAACGATGGGTG
 GATCGTAGAGCGTGAACGCTCGCTGCCATCTTGCTCCGGTGTGGGAGAGGAATACCCATGGCGGCC
 AGTCGCGCCAGATAGCGCTAGTCGCTCTCCCGCGCCGCTACGTCAGCGCTCTGAATCTCGGAGCGTCTGCC
 TACCGACTGAGGCTGTGCGACCGCGCAGAAGGGTTGAAAAAGCCCATCAATAGTCCTCCGTGCGTCCGGCG
 GCGTACTGGACTCGCTGGTAGAAGGGAACACGGTGGTAGCCGGTACCGGGCGGGATCGTGCCTGGCCAGGTGCG
 GGAACACATACATCACCAGGTGGGATTGGGAGTCGTTGAATGACTGTGGATCTCGTGTGGCGTGGGGTGTAG
 TCGGCCTGGTCAATTGGCGAGGCATCCTGCTCGGGATCGATTGGCGCCGCAGCGTTGCTGGCATCGAGGAGCAGCC
 GCCACGGCTGTTGCCTATCGAGCTGGTCGACCTCGCTCCAGACGTCGAGCATGTTGGCCTCGCCGTGGGGCAGCATCT
 CCTCCTGCTGGTGGAGCACGCTGCCAGGGTCAGCGCGCAGGCCGGCGAGAGACGAAGAAGGGGGTAGTC
 GTCTGCTGTTGCATGAGCGGCTCAGAGCTGAATGACCTGCGGGCCCTGA

>ORF594 (SEQ ID NO:12)

CCAGGGCAGACTACACCCGCACGGCCAGCAACGAGATCCACAGTCAGTTCAAACGACTGCCCAATCCGACCTGGTGATGT
ATGTTCCCGCACCTGGCCGGAGCGATCCCGCCCCGGTACCGGGCTACACCACCGTGTTCCTCTACCGAGCGAGTC
CAGTACGCCATGCCGGCGAACGCACGGAGGACTATTGATGGGCTTTTCAAACCCCTCTGCAGGGTGCACACAGCCT
CAGTCGGTACCGGCAGACGCTCCCGAAGATTCAAGGAGCGCTGGACGTAGCGGCCGGAAAGAAGCGACTGAGCGCTATCT
GGCGCAGCTGGCCGCATGGGTATTCCCTGCACACCCGGAGCAAGAATGGGCCACGCAGGCCAGAGCGTACGCC
TCTACGATCACGACCCATCGTCGTAGACCTGCTGCCCTGGGCTGAGTACCTGCCGACGAGCAAGTGTGCTCTGGAG
GATGGGCGTTCGCGCCCGCATTCTCGAACCTGGTGCCTGGGACCCGAGGGCGGATCCAAATTGGATGCGAGAACGC
CCGGGACGCATTGAAAGAACGCCCCGAGAACCTCCAGGAGCAGTTGAGGAGCTACGTCCATCTCGAGCGCAGGGATCGGCCCTCAGC
AGGACGAGATCAGCTGGGACAATTCCAGGAGCAGTTGAGGAGCTACGTCCATCTCGAGCGCAGGGATCGGCCCTCAGC
GAGATGTACCTGGCGCTCATGAAGCATCACCTGGAGGGCATTCGAAGGCCGGGACTGTGTCGACACCGCCGTCA
CAAGCTGCCCTGGCGAGGACAAACAGCGCCGGTGCAGGATGGTCGTCTACCGCCGGATCCGCAAGGAGGATGCGCAGATT
GCGGACAGGACCCGGCGCGTACCTGAAATCCATCTCGAGCGTATCCAAGGCCGGCTGGCGAACGCCGGCATCGTCGCT
TCGCGATGGCGGACAGGAGATCAGGAACCTGGTGTACCGCTGGTCAACCCGACCCGGATCACCTGCCAGGGCGA
GGCGGACCTACGTGCTTCTACGAACCTGGTATGCCGTCCGGACGAACCGATCTCGAGGATGAATTGCCACTGGCCAGG
GCACTGACTTCTCCCAGAACCTGTTCTATCGGAGCGCTGGTCTTCGATGCCACCCAGGGCGTATGGCTCTCGATGCCATG
CCGCACCGAGTGTGTTGGTCGACCGAGTTGAACAAAGGCCGGTACAGGCCACCCGGTCAACCGCAGGCTCAAAGCGA
TGGCCTCAACGCCCTGTCGATCGAACGCCAGGACACGCTGTCGATCACCATGGTGTGACGCCAGGACATGC
TGGAAAGGCATCTGAGCAGCTCGAAAAAGGCCGTTGGTACACCCAGGCCCTGATCCACACCCGCCAGGACGCTGGCC
ACCGTTGACGCCGTATGGCCGGAGCACAAGCTCTATCGGGAGCGATCGCTCTGTTGCGCGGCCGACCCATAC
CCAGTTGGAGGAACGCTGATCACCTGAGCAACGTAACGCTACTGCTCGGCCGGCTGGTGCCTGCAACCGCAGAACCGAAG
TCGGACCGCTGAAACAGCTACCTGCGCTGGCTCCCCTCAACCTCGATCCAACCGAGAAGCGAGCCCTGGAGTGGTACACC
CAGATGATGTTGCTCAGCACATGCCAACCTGTCGCCATCTGGGGCGCACACCGGTACCGGACACCCGGTCA
GCTGTTCAACCGTGGCGCGCCGGTGTGACCTCGACCCGTTCAACAAGCTGGACCGGAGATGAATGCCACGGCTTCA
TCTCGGGCCAACCTGGCTCCGGCAAGTGGCGTCCCTGACCAACCTCATCTGCCAGATGCTGCCATGTA
ATGTTGCTCGCGGAAGCGGGCACAGCTCGGCTGCTGGCGACTTAGCCAAGCGGTTGGCCTCTGGTCCACCGGGT
GCGCCTCGCCCCGGGCTCCGGCGTCAGCCTGGCGCGTGCAGGCCATCAAGCTGGTCAAGAGGCCGACCAAGTGA
AGGTGCTGGACGCCGAAGACATCGAGGCCTCGGACTCGGTCCAGGGAGCAAGGCCACCTCGAGGAGCACCAGCAGAC
ATCCCTGGCGAGATGGAGATGTCGCCGCTCATGATTACCGGTGGAGAGAGAAGGAAGATGCGCGCTGACCCGTG
CGATCGCAGCGCCGTCGCCAGCGATCTGGCGGGCAGGACCTGCGCCGCCGAACCGCACGGTACTGACCAAG
ACGTGCGCGATGCGCTCTACGAGGCCTCCAGGAGCGATAGCACCGCGCCAGAACGCCGCGCGGATGCCGAAATGGCG
GAAGCCATGCGAGATGTTCTGCAAGGGCGCCAGGGAGATGTTCAATCGCGAAGGACGCCCTGGCTGAGGCCGACCT
TACCGTGGTGGATTTCGCAACGTACGCGCGGAAGGCTACGCCGCCAGCTCGGGATGCCATCTCGCTGCTGAACA
CCGTGAACAAACATGCCGAACCGGACCGAGTTCAAGGGCGCCAACTCGTCAAGATCACCGATGAGGGCACATCATCACC
AAGCACCCGCTGTCGCTGCCCTACGCCATGAAGATCACCAAGATGTGGCGGAACTGGGCCCTGGTTCTGGCTGCCAC
CCAGAACATCGACGACATCCCAGCCTCCGGGGCGCCAGTGTGAACATGATCGAGTGGTGGTGTGCCCTGAACATGCC
CCGACGAAGTAGAGAAGATATCCAGGTTCCCGCAGCTGTCGCCGGCGAGAACGTCGATGATGCTCTCGGCCGCAAGGAA
AGCGGCAAGTTCACCGAGGGCGTCCTGCCAAGGGCAAAAGAATACCTCGTCCGTGTGGTCCCCCGAGTCTACCT
GGCCCTGCCATGACCGAAAACGAAGAAAAGAACCGAGCGCTACAAACATCATGCAAGGCCACCGCTGCGACGAGCTCGAGG
CGGCCCTTGCAAGGTCGCGAGCGGATCTCGACAAGGCGCGCCGGCTGCCACCCCTCCCCATTGTTTCCCAGACCAACGGGCA
GTGGAGTGCAGGAGCAATGA

>ORF1040 (SEQ ID NO:14)

GTACCTGGCCGACGAGCAAGTGTCTGGAGGATGGCGTTCGCGCCGATTCTCGAACTGGTGCCTTGGGCA
CCGAGGGCCGCGATCCAATTGGATGCAGAACGCCGGGACGCATTGAAAGAACCCCTGCAGAACTCCTCGACGAGCAC
GAAACCTACCCCTGGATTGTCCAGTTCTACGCCAGGACGAGATCAGCTGGGACAATTCCAGGAGCAGTTGAGGCAGTA
CGTCCATCTCGAGCGCGAGGATCGGCCTTCAGCAGATGTACCTGGCGCTATGAAGCATACCTGGAGGGCATTCGA
AGCCGGGCGGACTGTTCTCGACACCGCCGTCAAGCAAGCTGCCCTGGCGAGGACAACAGCGCCGCGTGC GGATGGT CGTC
TACCGCCGGATCCGCAAGGAGGATGCGCAGATTGCGGACAGGACCCGGCGGTACCTGAATCCATCTGCAGCGTAT
CCAAGGCGGCTGGCGAACGCCGGCATCGTCGCTTCGCCATGGGCGGACAGGAGATCAGGAACCTGGTATCCGCTGGT
TCAACCCGACCCGGATCACCTCGGCCAGGGCAGGCGGACCTACGTCGTTCTACGAACCTGGTATGCCGTCCGGACGAA
CCGATCTCGAGGATGA

Fig. 3-2

>ORF1640c (SEQ ID NO:16)

GTCCGCCTCGGCCTGGCGAGGTGATCCGGGTTGCGGGTTGAACCAGCGGATCAACCAGTCCCTGATCTCCGTCCGCCA
 TGCGCGAAGCGACGATGCCGGCTTCGCCAGGCCCTTGGATACGCTCGAGATGGATTCAAGGTACGCCGCCGGTCC
 TGTCCCGGAATCTGCCATCCTCCTGGGATCCGGCGGTAGACGACCATCCGCACGCCGCTGTTGTCCTCGCCAGGG
 CAGCTTGTGACGGCGGTGTCACGAACAGTCCGCCGGCTCGAAATGCCCTCAGGTGATGCTTATGAGGCCAGGT
 ACATCTCGCTGAAGGCCATCCTCGCTCGAGGATGGACGTACTGCCCACTGCTCCCTGAAATTGTCCCAGCTGATC
 TCGCCTGGCGTAGAACTGGACAATCCAGGGTGA

>ORF2228c (SEQ ID NO:18)

GGGGAGCCAGCGCAGGTAGCTGTTAGCGGTCGACTTGTCTGCCGACCGGGCACCAGGCCGGCGAGCAGTA
 CGTTGCTCAGGGTATGCAAGCGTCTCTCAACTGGGTATGGTCGCCGCGCAGAACAGAGCAGTCGCTCCCGCATAG
 AGCTTGTGCTCCCGGCCATCAGCGTCGAACGGTGGCACGTCCTCGCGGGTGGATCGAGGCCCTGGGTGTCACCAAC
 GGCCTTTTCGAGAGCTGCTGCAAGTGCCTTCCAGCATGTCCTGCCGTCACGACCATGGTATGCAAGCAGCGTGT
 CCTCGGGCATTGATCGAACAGGGCGTTGAGGCCATGCCCTTGAGCGTCTGCCGGTGAAGTGGCCTGTCAGCGGCCCT
 TTGTTCAACTGGTCGACCAAACTACTCGGTGCGGCATGGCATCGAAAGGCCATACGCCCTGGGTGGCATCGGAAACAGG
 CTGCCGATAGAACAGGTTCTGGAGAAGTCAGTGCCTGCCAGTGGCAATTGATCGCAGGATCGGTCGTCGGAC
 GGCAACAGTTCGTAGAACAGCGACGTAG

>ORF2068c (SEQ ID NO:20)

AGCTTGTGCTCCCGCCATCAGCGTCGAACGGTGGCACGTCCTCGCGGGTGGATCGAGGCCCTGGGTGTCACCAAC
 GGCCTTTTCGAGAGCTGCTGCAAGTGCCTTCCAGCATGTCCTGCCGTCACGACCATGGTATGCAAGCAGCGTGT
 CCTCGGGCATTGATCGAACAGGGCGTTGAGGCCATGCCCTTGAGCGTCTGCCGGTGAAGTGGCCTGTCAGCGGCCCT
 TTGTTCAACTGGTCGACCAAACTACTCGGTGCGGCATGGCATCGAAAGGCCATACGCCCTGGGTGGCATCGGAAACAGG
 CTGCCGATAG

>ORF1997 (SEQ ID NO:22)

CACCCAGGCCCTGATCCACACCCGGAGGACGTGGCACCGCTGATGCCGGGAGCACAGCTCTATCGC
 GAGCGATGCTCTGTTGTCGCCGCCGACCATACCCAGTTGGAGGAACGCTGATCACCTGAGCAACGTACTGCTC
 GGCGCCGGCTGGTGCCTGCAACCGCAGAACGAGTCGGACCGCTGAACAGCTACCTGCCGCTGGCTCCCTCAAACCT
 CGATCCAACAGAGAACGAGCCCTGGAGTGGTACACCCAGATGATGTTGTCCTGACGACATGCCAACCTGTCGCCCATCT
 GGGGGCGCACCCGGTACCGACACCCCTGGCTTCAGCTGTTCAACCGTGGCGCGCCGTTGACCTTGACCCGTT
 AACAAAGCTGGACCGCAGATGAAATGCCACGGCTTCATCTCGGGCAACTGGCTCCGGCAAGTCGGCTCCCTGACCAA
 CCTCATCTGCCAGATGCTGCCATGTACCTGCCGCGGATGTTGTCGCGGAGCGGGCAACAGCTTCCGCTGCTGGCC
 ACTTAGCCAAGCGGTTGGCCTCTCGGTCCACCGGGTGCCTGCCCTGCCCGGGCTCCGGCTCACGCTGGGCCGTTGCG
 GACGCCATCAAGCTGGTCGAGAGCCCCGACCAAGTGAAGGTGCTGGACGCCGAAGACATCGAGGCCCTGGACTCGGTCCA
 GGGCAGCAAGGCCGACCTCGAGGACGCCAGCGAGACATCTGGGCGAGATGGAGATGTCGCCGCTCATGATTACCG
 GTGGCGAAGAGAAGGAAGATGCGCCTGACCGTGCCTGACCGATCGCAGGCCGTCGCCAGGCATCTGGCGCGGCCAGG
 ACCTGCCGCCGCCGACCCGACGGTACTGACCCAAGACGTGCGCAGTGCCTGCGCTACGAGGCCCTCCAGGAGCGATAG

>ORF2558c (SEQ ID NO:24)

GTCGGCCAGCAGGCCGAAAGCTGTTGCCGCTCCGCAGCAACATCCGCCAGGTACATGGCGAGCATCTGGCAGATGA
 GGTTGGTCAGGGACGCCGACTTGGCGAGCCAGTTGGCCGAAGATGAAGCCGTTGACCGTGGCATTGATCTGCCGCTCAGCTTG
 TTGAACGGGTCGAAGGTCAACGCCGCCACGGTTGAAACAGCGTGAAGCCAGGGTGTCCGGTACCGGTTGCGGCC
 CCAGATGGCGACAGGGTTGGCGATGTGCTGAGCGAACATCATCTGGGTGTAACCACTCCAGGGCTCGCTTCTGTTGGAT
 CGAAGTTGA

>ORF2929c (SEQ ID NO:26)

AGCGCATCGCGCACGTCTGGGTCAAGTACCGTGCAGGTTCGCGGCCAGGTCTGGCCCGCCAGGATCGCCTGGCG
 GACGGCGCTCGATCGCACGGTCAGGCGCATCTCTCTCTCGCCACCGTAATCATGAGGCAGGCGACGATCT
 CCATCTCGCCAGGATGTCTCGCTGGTCGCTCGAGGTCGGCCTGCTGCCCTGGACCGAGTCCGAGGCTCGATGTCT
 TCGCGTCAGCACCTCACTTGGTCGGGCTCTCGACCAGCTGATGGCGTCCGGAACGGCGCAGGCTGACGCCGA
 GCCCGGGCGAGGCGCACCGGTGGACCGAGAGGCCAAACCGCTTGGTAAGTCGGCAGCAGGCCGAAGCTGTGCCG
 CTTCCGCAGAACATCCGGCAGGTACATGGCGAGCATCTGGCAGATGAGGTTGGTCAGGGACGCCACTGCCGAG
 CCAGTTGGCCGAAGATGAAGCCGGGGATTCACTCGCCGTCCAGCTGTTGAACGGGTCAGGTCAGGTCAGGCC
 GCCACGGTTGAACAGCGTGAAGCCAGGGTCCGGTACCGGTGGTGCGCCCCAGATGGGCAGAGGTTGGCAGTGTGCT
 GA

>ORF3965c (SEQ ID NO:28)

GCGCTGTGGCGTATCAGGCTGTGGATGTTGCAAGCATTCAAGAGCTGCCTTATCTGGGGACGATATCC
 CGGCGATCGACTGCCCTCAGTTGAATCTGCTGCAGCTCTATCAGTACAGGAGCGCATTCCTAGCGCTCGCAGGGC
 ATCCTCTCGGGGTTCTGCAGGATCTGGGTCAAGGTTGTCAGGTTCTGGGTCAAGCGAATTCAAGAACCTCTATTGTC
 CTGGCACTCCACTGCCGGTGGTCTGGAAACAAATGGGAAGGGTGGCAGGCCGCGCCTGTCAGGATCCGCTGCGA
 CCTGCAAGGCCCTCGAGCTCGCAGCCGGTGGCTTCAGTGTAGCGCTGGTTCTTCCTCGTTGGCAGGAGCACGCCCTCGGT
 ATGGCCAGGGCAGGTAGAGACTGGGGAACACACGGACGAGGTATTCTTGCCCTGGCAGGAGCACGCCCTCGGT
 GAACTTGCCTTCCCTGCGGGCGAGAGCATCATGACTCTGCGCCGGCGACAGCTCGCGAACCTGGATATCTTCT
 CTACTTCGTGGGGGCGATGTTCAAGGACAACCAACACTCGATCATGTTCAAGCATCGGCCGGCGAGGCTGGGATGTC
 TCGATGTTCTGGGTGGCGAGCCAGAACCCAGGGCGCCAGTTCCGCCACATCTTGGTATCTTCATGGCGTAGGGCAGCAG
 CAGCGGGTGTGGTGTGATGATGTCGGCTCATCGGTGATCTGACGATTGGCCGCCCTGAACTGGTGGCTTCGGCGA
 TGTTGTTACGGTGTTCAGCAGGGAGATGTAAGCGATCCCGAGCTGGCGGTAGCCTTCGCGCGTACGTTGCGAAA
 TCCACCACGGTAAGGTCGGCCTCAGGCCAGGGCGCTTCAGCGATTGAAACATCTCGCGCTGGCGCCCATGAGAACAT
 CTGCATGGCTTCCGCCATTGCGGATCCGCGCGCGCTTCTGGCGCGGTGCTATCGCTCTGGAGGCCCTGAGAGCG
 CATCGCGACGTCTGGGTCAAGTACCGTGCAGGCGTCCGCGCGCAGGTCCTGGCGCCAGGATCGCCTGGCGGACG
 GCGCTGCAGTCGGCACGGTCAGGCGCATCTCCCTCTCGCCACCGTAATCATGAGGCGGGCGACGATCTCCAT
 CTCGCCAGGATGTCTCGCTGGTCGCTCGAGGTCGGCCTGCTGCCCTGGACCGAGTCCGAGGCCCTGATGTCTCGG
 CGTCCAGCACCTCACTTGGTCGGGCTCTCGACCAGCTGATGGCGTCCGCAACGGCGCAGGCTGACGCCGGAGCCC
 GGGCGAGGCGCACCGGTGGACCGAGAGGCCAAACCGCTTGGCTAA

>ORF3218 (SEQ ID NO:30)

GGGGCACATCATCACCAAGCACCGCTGCTGCCCTACGCCATGAAGATCACCAAGATGTGGCGAAACTGGCGCCT
 GGTTCTGGCTGCCACCCAGAACATCGACGACATCCCAGCCTCCGGGGCGCGATGCTGAACATGATCGAGTGGTGGTG
 TGCCTGAACATGCCCGACGAAGTAGAGAAGATATCCAGGTTCCGCGAGCTGTCGCCGGCGCAGAAGTCGATGATGCT
 CTCGGCCCGCAAGGAAGCGGCAAGTTCACCGAGGGCGTGCCTCTGCCAAGGGCAAAGAACATCTCGCCGTGTT
 CCCCAGTCTCACCTGGCCCTGCCATGACCGAAAAGAACCGAGCGCTACAACATCATGCAAGCCACCGC
 TGCGACGAGCTCGAGGCGGCCCTGCAGGTCGAGCGGATCTCGACAAGGCGCGGCCCTGCCACCCCTTCCCATTGTTT
 CCCAGACCAACCGGAGTGGAGTGCAGGACGAAATGAGAGTTCTGAATTGCTGACCCAGAACCTGATCGACAACCTGAC
 CCAGATCTGCAGAACCCGAAGAGGATGCCCTGCAGACGCTAACGGATATGCGCTCTGACTGATAGAGGAGCTGAGC
 AGATTCAACTGAGGGAGTCGATGCCGGGATATCGTCCCGCAGATAAAGCAGCTTGGATGAATGGCTGCAACACAT
 CCACAGCCTGATAAGGCCAACAGCGCTATTGAGGCCGTGGACCGCGGAGATCCTACAGCGGAGGCAAGCGTGA

>ORF3568 (SEQ ID NO:32)

CCGAAAACGAAGAAAAGAACCGAGCGTACAACATCATGCAAGCCACGGCTGCGACGAGCTCGAGGCGGCCCTGAGGTC
 GCAGCGGATCTCGACAAGGCGCGGCCCTGCCACCCCTCCCCATTGTTTCCAGACCAACCGGAGTGGAGTGCCAGGA
 CGAACATGAGAGTTCTGAATTGCTGACCCAGAACCTGATCGACAACCTGACCCAGATCCTGAGAACCCGAAGAGGATG
 CCTGCAGACGCTAACGGATATGCGCTCTGACTGATAGAGGAGCTGAGCAGATTCAACTGAGGGAGTCGATGCCGG
 ATATCGTCCCGCAGATAAAGCAGCTTGGATGA

Fig. 3-4

>ORF4506c (SEQ ID NO:34)

GTCAATAAGTCGTTGCTTCGACATTTCTCCAGTCGAGCCTGGTCCAGTCAGGAAAGTCCAATGTGCCGCCAGGCA
 GCCCGCCCCCGTTGCCGCCAGCTGAGCGAAGATCGCATCGATAGCGCTCCAGAAGGCTTGGGCCGCTTGGATCCCC
 GCGCACTCACCAGGCAGCCTGGTGGCGGGCGCCTGCCATGCATCTGCAGGGGAAGATGGGCCAAACCAGGTTCAC
 GTCCGGATGGCTGTCTACCCAGCGCTTAAGCCGGGGTGTAGACCTTGAGAAGGGGACTCCAGGTGGCTATTCAT
 TGATCGTCAGCGCGCTTCGATCGCGTAAGGGCTGTTGGCTGGCAGGCCCTCACCAAGAGCTCACCCCTACG
 GCGGATGCAGCCAGCAAGACCAGCAGCAGCCCCGCCAGGGCAGGGGGACCTTGAAATCGTTGGCTGCCAGCCGCC
 CTTCAAGAGTCTCACGCTTGCCTCCGCTGTAGGATCTCCGCGGTCCACGGCCTCAATGAGGCCGTGGGCCGTATC
 AGGCTGTGGATGTTGTCAGCCATTCAAGAGCTGTTATCTGGGACGATATCCGGCGATCGACTGCCCTCA
 GTTGA

>ORF3973 (SEQ ID NO:36)

GGCGGTGGACCGCGCGAGATCCTACAGCGGAGGAAGCGTGAGACTCTGAAGGGCGGCTGGCAGCCAAACGATTCA
 AGGTCCCGCCCTGCCCTGGCGGGCTGCTGCTGGTCTTGCTGGCTGCATCCGCCGTAGGGTAGAGCTCTGGTGAAGG
 GCCTGCCAGCCAACCACAGCCTCTACGGCGATGCGAAAGCGCGCTGGACGATCAATGAATACGCCGACCTGGAGTGCC
 TTCTGCAGAGTCTACACCCCCGGCTTAAGCGCTGGGTAGACAGCCATCCGGACGTGAACCTGGTTGGGCCATCTTC
 CCTGCAGATGCATGGCGAGGCGGGCCACCCAGGCTGCCCTGGTGGAGTGCAGGGGGATCCAAGGCGGCCAAAGCCT
 TCTGGAGCGCTATCGATGCGATCTCGCTCAGTCGGCCGCCAACGGGGCGGGCTGCCCTGGGGCACATTGGACTTTCT
 GAACTGGACCAGGCTCGACTGGAGAAATGTGCGAAAGACAACGAACTATTGACTCAGATATCAAGTTGGACATCGACAT
 TGACGGTCAAGGGCATTACAGCGACCCGACCCCTCGTATCCGGGACAACCAGACGGGACAAGCGTGAAGCTTGAAG
 GCATGGCCGACGAGACACGTTGCTGGCGATAGACTGGCTAGCCAAGGATCTCTAG

>ORF4271 (SEQ ID NO:38)

ACCTGGTTGGGCCATCTCCCCCTGCAGATGCATGGCGAGGCGGGCCACCCAGGCTCGCTGGTGGAGTGCAGGGGG
 ATCCAAGGCGGCCAAAGCCTCTGGAGCGCTATCGATGCGATCTCGCTCAGTCGGCCGCCAACGGGGCGGGCTGCC
 TGGCGCACATTGGACTTTCTGAACCTGGACAGGCTGACTGGAGAAATGTGCGAAAGACAACGAACTTATTGACTCAG
 ATATCAAGTTGGACATCGACATTGCACGGTCAAGGGCATTACAGCGACCCGACCCCTCGTATCCGGGACAACCAGACG
 GGACGAAGCGTGA

>ORF4698 (SEQ ID NO:40)

GAAATCGCGAGGATTCAAACATCCCTTTGGCTCCAGGATGCCCTGCACTTCACCTGGCAGAACCTCGACCTCCT
 CCCCATCCACAATCTTACCATTTCTTGTGGCCGGAGCTGGTGGGCTAAGCCTCACTCCATTGCCGGCGAGCATTG
 ATGTAATGCTCTCGAGCAAGCGCTCCATGACTCGACCACTCCTAATATCAGTTAGCCAGTACATAACAGGAAATTATG
 CTACCCAGGACATGCAGCGTCACCCCTACTTATGTACGTGGCAGCGTCAACGGCTCGAAAAAAATACACCCACCTAC
 GAGTTGA

>ORF5028 (SEQ ID NO:42)

TTCCCTGCTGCCCTATCGGAAGTGTCTGCTGCTGTACCTTCTAGAACCGGTACAGACCCATGCCCTTCATC
 ACTCCCCCTGGCCGGGCCACCAACGCTGGCGTTGGCTACTACTGGTACTGCTGAGCAGCGAGTCAGGCCAA
 ACCTGGGTCACTACCGACAAGGCTCATCCGGCTCTGCCACCGGATCGCGCGTTCTGTTCTGGACGCCAGGAACA
 CCTCGAGGAGCAACTGACTGCCCTTGGCCAGGATCCACAGCATGCTCAAGCGCGTTAA

>ORF5080 (SEQ ID NO:44)

AACCGGTACAGACCCATGCCCTTCATCACTCCCCCTGGCGGGCCACCAACGCTGGCGTTGGCTACTACTGGT
 ACTGCTGAGCAGCGAGTCAGGCCGAAACCTGGTCACTACCGACAAGGCTCATCCGGCTCTGCCACCGGATCGTCGC
 GCGTTCTGTTCTGGACGCCAGGAACACCTCGAGGAGCAACTGACTGCCCTGCCACAGGATCCACAGCATGCTCAA
 GCGCGTTAAGCGATTGCTACAAAGCCCCGATGGCGGCCCTGCAGGCAGAGCTGGTCAAGGCACAACAAGACGTCGC
 CGATGCGTGGAGTCTGGTGTGAGAAGATCCCTGCCGTAGTAGTCGATAGGCAGTACGTGGCTACGGGAACCGGATG
 TTGCGCGCTTGTAGCTAATGCCAAGGCCAGGAGGTCGCGCTGA

Fig. 3-5

>ORF6479c (SEQ ID NO:46)

TTCGTCTCGTGTCTTATTGGAAGTCGGTACTGCAGATGAACATCTGCCCTTGCCTGGCAGCAGGAGTAGGGACGCC
 AGAGCGCCCAGGCGTGTCTCCCGTCAGCGCTTGCCTCGGCCAGAGTTGGAAACACCGCGCAGTTGAGGCTCAGG
 GATGGGGTCAGCTCTGCCATTCCCGTCAGGCATGCCCTTTCACTCGCCGGCCAGTAGCCGTCTTGGCGATATGCCGGCGCTGGG
 GGCTGCGCATGGGAGGTAGACGTGGAGCTGGCGATTCGCGTGGTATATGCCGGCGCTGGCGATGACGGCTG
 CGCTTGTAGTCGTCGGTCTGGTCAGGAAGCCGCTGCCGGATAGAGTTCCCCACATGTCGCCGGAGAAGATTCCA
 CCCACCTCGCGCAGCCCTGGGACCAACGCTTGGGTACACCTGCTCGGAATTCCATGCCGCCAGCCAATGGCGTCCAG
 TGTGCTGAGAAAGTACGGCACCAAGCGGGACGGTGGCGCAGGGAAACGTACCCAGAGGCGTGGCGAACCGGCTGAACG
 TGGCGCACCAGGATGGCGATCACATCCGCTTCTTGAAAGCGCCGATGCTGTTCTGGCTTGTAGTTGTGGTCGG
 TCATTGCCGCTGGCGAGTGGATTGGTGTACCCAGCGCCGATACCTCGGTCCAGGGTTGCTCCGGTATTGCGTA
 GCTGGAGACGACTCGGTCAAGGACGCTAGTGGCGACCTTGACCGACGTCTTCACTTGAGCCATGCCGGCGCAGAGCA
 GCCAGTAACAGATCCCACGACCTGTATTGAGGCACTGAGGGGAAAGGGTGGAGGAGACGATGGCAGCGTGTGATC
 GCGGCCGAGGCGTGAACGAGGGCTGAAGGGGGCCGCTGCCAGGGGGAGGGTTGAGGCTGGTATCAGCGC
 GACCTCTGGCTTGGCATTAGCTAAGAGCGCGAAACATCCGGTTGCCGTAG

>ORF5496 (SEQ ID NO:48)

GCTAATGCCAAGGCCAGGAGGTCGCGTGTGACCAGCCTAACCTCCGCCCTGGCAGCGCCGCCACCTTCAG
 CCTCTCGTTACGGCTCGGCCGATCAACAGCGCTGCCATCGTCTCTCCACCCCTTCCCTCAGTGCCTCGAATACA
 AGGTGCTGGGATCTTACTGGTGTCTGCCCGCATGGCTGCAAAGTGAAGACGTCGGTCAAGGTCCGCCACTAC
 GTGCCCTGACGCACTCGTCTCCAGCTACGCAATACCGGAGCAACCCCTGGACCGAGGTATGGCCTGGGTACACCGAA
 TCCACTCGCCAGGCCGCAATGACGCAACAAACTACAAGGCCAGAACAGCATGGCCCTTCAAGGAAGCGGATG
 TGATCGGCCATCTGGTGGGCCACGTTAGCCGGTCCAGCGCTCTGGGTACGTTGCCCTGGGCCACCGTCCCG
 CTGGTGCCGACTTCTCAGCACACTGGACGCCATTGGCTGGCGCATGGAATTCCGAGCAGGTGTACCCGAAGCGTT
 GGTCCCAGGGCTGCGCGAGGTGGGAATCTCTCCGGCAGATGTGGGGAAACCTATCCGCGCAGCGGCTTCTGC
 ACCAGACCGACGACTACAAGACGGCAGCGTATGCCAGCGCCGGCGATATCACCACGCAATGCCAGCTCCAC
 GTCTACCTCCCCATGCGCGAGCCCCAAGGACGGCTACTGGCCGGGGCGAGCTGAAAGAGGGCGATGCCCTGACCG
 GAAATGGCAGGAGCTACCCCATCCCTGAGCCTCAACTGCGGGTGTTCCTCAACTCTGGGCCAGACGCAAGCCGTG
 ACGGGGAGCACGCTGGCGCTGGCGTCCCTACTCCTGCTGCCAGCGCAAGGGCAGATGTTCATCTGCACTGAC
 TTCCAATAA

Fig. 3-6

>ORF5840 (SEQ ID NO:50)

CGCGACCACAAACTACAAGGCCGAGAACAGCATCGGCCGCTTCAGGAAGCGGATGTGATGCCATCCTGGTGGCGCCA
 CGTTCAGCCGGTCGCCAGCGCCTCTGGTACGTTGCCCTGGGCCACCGTCCCGCTGGTGGCGTACTTCTCAGCAC
 CTGGACGCCATTGGCTGGCGCATGGAATTCCCGAGCAGGTGACCGTGGTCCAGGGCTGCCGAGGTGG
 TGGAAATCTTCTCCGGCGACATGTGGGGGAAACCTCTATCCCGCAGCGCTTCCCTGCACCAGACGACTACAAGACGG
 CAGCCGTATCGCCAGCCGCCGGCATATCACACCGCAATGCCAGCTCCACGTCTACCTCCCCATGCCGCCAGCC
 CCCAAGGACGGCTACTGGCCGGCGGGCGAGCTGAAAGAGGGCGATGCCCTGACCGGGAAATGGCAGGAGCTGACCCCATC
 CCTGAGCCTCAACTGCGCGGTGTTCCCAACTCTGGGCCAGACGCAAGCCGTCAGCGCTGGGAGCACGCCCTGGCGCTCT
 GGCCTCCCTACTCCTGCTGCCAGCGCAAGGGGAGATGTTCATCTGCACTTCAATAAGGACACGGAGACGAA
 TCATGCGAATGAACATCACCTCGGTCGCTAATGTGGCTGCTCGCAGCGCAACTGCCAGGCCAGCACCGATCAAC
 GTGTCCAAGACGGCACGGTGTCAAGCAGGCTCTACAGCATTGGCGGCCAGTGGGTGAGCATGGCAGCG
 CGGCCAGATGGACTCGATGGCTCGGCTTGGCTGGAACACGACATGATGTGGAAACATGAAACCTGAGCACCA
 TGGAGAACACGCTAACGGTGCCACAGGGTTCCAGAACATCATGGCTCAGTCATCCAGAACGCGACGGCGCG
 ATGTCGCTGCCGGCTTGATCATCCAGCGCGAACCTCAGCTCTACAAACCTGATCACCAATGGCATCTGCAGGCG
 GATCGACTACGACCGCTCGAAAGGGACTTGAAAACGATGCCGAAAGATGGCTGACATCGCTGGCGAGCAGACGGCT
 GGGGAAATCGCGAAGGCCAACGGCTGGCGCACACTGGCTCTGACGGGAAAGACGCCGATCCGCGCTCGAAGCA
 GTGGAGAACAGGCGAACGATGGCTAACCTGGGTTGGAGACAAGGCCGGCTCCGGCCAGAACGCCATTG
 CATCGTCAACGACGTGACCCGGGGCTACAACCTGTTGACCGCCGTCGGTGAATGATTGTCGAGCGTGCCTTCG
 CCACTTGCAACAACGGCTGGTCTGCAACACTTGGCTCTCCCCCAGGAGGCCGCGATTGCCACCCGGTACTGGG
 GAGCAACAGCAACAGACACTGCGAAGGCTGCCAGAACGCGTACGGCTGCTGGCGTCGGCTCACCCGCTGATCCAGGA
 GACCTACGACAAGAACGCTCAGTCGCTGCGAGGCTGCTGCAAGAGCAAACCAACTGACTGAGAGAACCTGGCTGCG
 CGGGCACCGATGCTGCCAATTACCCGCGGCGTACGAGGCGTCGCGACGAGCGTGACCGAGCTCTGGCGCG
 CGCCTGGCGTCCGATGTCCTCTGATGGACGTGCTCAGCAAGGCACTGCTACTGAGCGCTGATGTTGCCGGCGCAA
 GGAGCCAACGTCGCCAACGGCTGGCACCCAGCGTCATCAGCAGAACGCGCTCTGCAGCAGGAGATCTCCA
 ATCTCAAGACCGAACTGGAACTCCGTCGAGTTGGCAGCAACTCCCCATGCGGGTATCGAGCGCGGGCAACACG
 GCCTCAGGGTCCAGTGGCGTGTGAGTCGGCGCCGATGCCGATGCCCTGATGCCCTGAGGCCCTCTGCCGCCGG
 CGGCAAGTCGGAGGGAGACCGTGA

>ORF5899 (SEQ ID NO:52)

TCGGCCATCCTGGTGGCGCACGTCAGCCGGTTCGCCAGGCCCTCTGGTACGTTGCCCTGGGCCACCGTCCCGCTG
 GTGCCGTACTTCTCAGCACACTGGACGCCATTGGCTGGCGCATGGAATTCCCGAGCAGGTGACCGAAGCGTTGGT
 CCCAGGGCTGCGCGAGGTGGTGGAAATCTTCTCCGGCACTGTGGGGAAACCTCTATCCGCCAGCGGCTTCTGCACC
 AGACCGACGACTACAAGACGGCAGCGTACGCCAGCGCCGGCATATCACACCGCAATGCCAGCTCCACGTC
 TACCTCCCCATGCGCGAGCCCAAGGACGGCTACTGGCCGGCGGGGAGCTGA

>ORF6325 (SEQ ID NO:54)

GCCTCAACTGCGCGGTGTTCCAACTCTGGCGAAGACGCAAGCCGTCAGGGGAGCACGCCCTGGCGCTCTGGCGT
 CCCTACTCCTGCTGCCAGCGAAGGGCAGATGTTCATCTGCACTTCCAATAAGGACACGGAGACGAATCATG
 CGAATGAACATCACCTCGTGCCTGCGTAATGTGGCTGCTGCCAGCGCAACTTGCACCGCCAGGCCGACGACCGATCAACGTGTC
 CAAGACCGCACGGTCTCGCGACGAGGTCTACAGCATTGGCGCCGGCAGTGCCTGAGCATGGCAGCGCCGGCC
 AGATGGACTCGATGGCGTCGGCTCGGCTGGAACACGACATGATGTGCGGAAACATGAAACCTGAGCACCCCTGGAG
 AACCAAGCTAACGGTGCCACACAGGGTTCCAGAACATCATGGCTCAGTCATCCAGAACGCGACCGGGCGGGTATGTC
 GCTGCCGGCGTGTGATCATCCAGCGCGAACCCCTCAGCTCTACAAACCTGATCACCAATGGCATCTGCAGCGCGGATCG
 ACTACGACCGCTCGAAAGGACTTGCAAAACGATGCCGAAAGATGGCTGA

Fig. 3-7

>ORF7567c (SEQ ID NO:56)

CAGTGCCTGCTGAGCACGTCCATCAGGGAGACATGGACGCCAGGCCGGCGCCAGGACGTCTGGTCACGCTCGTCGC
 GCAGCGCCTCGATGACGCCGGTAATTGGCAGAGCATCGTGCAGGCCAGGTTCTGCAGTCAGTGGTTG
 CTCTTCGACAGCAGCTCTGCAGCAGCTGGAGCTTCTGCTAGGTCTCCTGGATCAGCGGGGTGAGGCCACGCCAGC
 AGCCGTACCGTCTCTGGCAGGCCCTCGCAGGTCTGTTGCTCCCTGGATCAGCGGGGTGAGGCCACGCCAGC
 CCTGGGGGGAGGACCAAGTGTGAGACCAAGGCCGGTTGCAAGTGGCGGAAGGCCACGCCAGCAATCATTACCGAG
 CGGCTGGTCAACAGGGTAGCCGCCGGGTACGTCAGTGCAGATGCCAGGGCTTCTGGCCGGAGGCCCGGCCCTT
 GTCTCCACCAACCCAGGTTACGCCATCGTGCCTTCTTCTCCACTGCTTCGAGGGCGGATACGGCGTCTTCCCGT
 CAGAGGCCAGTGTGGCCGCCAGGGCTTGGCTCGCGATTTCCCCAGCCGGTCTGCTCGCCAGCGATGTCAGCCATC
 TTTTCCGGCGATCGTTTGCAAGTCCCTTCGAGCGGTCTAGTCGATCCGCGCTGCAGGATGCCATTGGTATCAGGTT
 GTAGAGCTGAGGGTTCGCGCCTGGATGATCAACGCCGGCAGCGACATGACCGCCGGTGCCTGGATGACTGA

>ORF7180 (SEQ ID NO:58)

TCGTCGAGCGTGCCTCCGCCACTTGCACAAACGCCCTGGTCTGCAACACTTGGCTCTCCCCCAGGAGGCCGCCAT
 TCGCCACCCGGTACTGGGGAGCAACAGCAACAGACCTGCGAAGGCTGCCAGAACAGCGGTACGGCTGCTGGCGTCGGC
 CTCACCCCGCTGATCCAGGAGACCTACGACAAGAAGCTCAGTCAGTGCAGGAGCTGCTGCGAAGAGCAAACCACTGAC
 TGCGAGAGAACCTGGCTGCCGCCGGCACCGATGCTCTGCCAATTACCGCGCGTATCGAGGCCTGCGCGACGAGCGTG
 A

>ORF7501 (SEQ ID NO:60)

CCAGGACGTCCCTGGCGCCGCTGGCGTCCGATGTCCTCTGATGGACGTGCTAGCAAGGCACTGCTACTGCAGCGCC
 TGATGTTGCCGGCGCAAGGAGCCAAACGTCGCCAACGGCCTGGCCACCCAAAGCCGTGATCAGCAGACCAGCCTC
 CTGCAAGCAGGAGATCTCAATCTCAAGACCGAACTGGAACCTCCGTCGAGTTGGCCAGCAACTCCCCATGCCGGTCA
 CGAGCGCGGGCAACAAACGCCCTCAGGGTCCAGTGGCGTGTGAGTCGGCGCCGATGCCGATGCCCTGATGCCCTG
 AGGCCCCCTCTGCCGCCGGCGCAAGTCGGGAGGGAGACCGTGATGGCAGATACTGCTCACCACCCGAAAGCTTCTCGGT
 AGCTACTGGTGGAGTGCTGATGTCATCGGACTGGCAGTGGTCGGTACGCTGCTAGTCTCTGCCCTGAACCACTTC
 GGTGGCATCCAGGGCTGGAGGCCGGCGAAAGCAACTACTGGAGCTTGTGCTGCCCTGGCGGGCTGCTGACTGCC
 CCTGGCCATGCCCTGGTCCGGCAGCGCAAGGAACTGAGCGCGATGAGCGGCAGCGATTGCCGGATCGAGATCCTGG
 TGCTGTTGCTGGTCTGCTCATCGAAAGCTACTTCCGACGGGAGGCCAGCGATGA

>ORF7584 (SEQ ID NO:62)

TGTTGCCGGCGCAAGGAGCCAAACGTCGCCAACGGCCTGGCACCCAAAGCCGTGATCAGCAGACCAGCCTCTG
 CAGCAGGAGATCTCAATCTCAAGACCGAACTGGAACCTCCGTCGAGTTGGCCAGCAACTCCCCATGCCGGTCA
 GCGCGGGCAACAAACGCCCTCAGGGTCCAGTGGCGTGTGAGTCGGCGCCGATGCCGATGCCCTGATGCCCTGAGG
 CCCCCCTCTGCCGCCGGCGCAAGTCGGGAGGGAGACCGTGATGGCAGATACTGCTCACCACCCGAAAGCTTCTCGGT
 TACTGGTGGAGTGCTGATGTCATCGGACTGGCAGTGGCGGTACGCTGCTAGTCTCTGCCCTGAACCACTTCGG
 GGCATCCAGGGCTGGAGGCCGGCAAAGCAACTACTGGAGCTTGTGCTGCCCTGGCGGGCGTGTACTGCC
 GGCCATGCCCTGGTCCGGCAGCGCAAGGAACTGAGCGCGATGA

>ORF8208c (SEQ ID NO:64)

AGGTCACTGCTGCCCTCCGTGCCGAAGTAGGCTTGCTGAATTGATGAGCAGGACCGAACAGCACCAAGGATCTGA
 TCCGCCGAATGCGCTGCCGTCATGCCGCTCAGTCCCTGCGCTGCCAGGCCACCGCGATGCCAGGGCGAGTACAGC
 AGCGCCCGCCAGCGAACAGCTCCAGTAGTGTGTTGCCAGGCCCTGGATGCCACCGAACAGTGGTCA
 GGCAGAGAGACTGAGCAGCGTACCGACCACTGCCAGTGCAGTCAGCACTCCGACCGAGTAG

Fig. 3-8

>ORF8109 (SEQ ID NO:66)

GGGGCAGCGCATTGGCGGATCGAGATCCTGGTGTGGTCTGCTCATCGAATTCAAGCAAAGCCTACTTCCGCA
 CGGGAGGCGCAGCATGACCTCATGACCAATGACTACCTGGAGTATTACCTCACCCCTCTGGCTGGATCATCAACAAACG
 GGATCTGGAACATGATCTGGATACTGGCCTGTTGGCGTCCGGCCATCGTGTGATGCGCGAATGGCTGAAAGTT
 CGTGGGGAAAGGCGCCGACGAGGGCAACAAGGGAGTGTCTCTGCCGCATCGAGACGCATATCTACGTCGGTACAT
 CGTGGTCCGCTGGGGGATCCCGGTCGTCAACGTGAGCTTCGACACCATCGAGTTGACCGAGACTCGGCCAGCAGT
 CGCAATAACATCTGCCCCACCGGGACACCCGCTGGTCAGCAGCCTGGCCGGCAAGAGTGCAGATG
 CCGCTCTGGTGGCGATGATGCACGCCGTGCAAGGGCTTCACCAGGGCCATCGCCGGCATTCCGTGCGGACCGA
 TCTGCGGCAAGATGCAATGGAAGTGGACAACACGCGCTGAAACAATCCGTCGTCGACAAGAAATCGCTGATTTTCA
 GAGACTGCTACGGGCTTCCCGTGCAGGCTGTTATGCGGCAACCGACCTGGGCTCCGTCGCCAGGGACAACAAGGCG
 TTGCAAGACCTGAACTGGATCGGCTCCGATTCTGTTGAAACACCCCCGGGTTACTACGACACCGACTACTCGAAGAGTCC
 CCGTCAGTCGTGGCCCTACAACGCCACCCCGCATGCCGCTGCCAGGTGGGCGGTGGTGGCGCTACCAACCTGCA
 AGCAGTGGTGGGCTGACTCAGGGATCGGCTTGGTGTGATCGGATCAAGGACCAAGGGTGGATCCGGACCTGATGAC
 CTCAGTGGCGAAATGGTGAACCAGGACGAGGTGACGGAGGCTGTCATTGCCAGGTGATCTCACCCCTCAGCCAGGT
 CAAGGGTAACGTCTACACGATTACGGCGGGCAGGTGGGCGCACCGTGTGGAACGGCATCGCGAGAACCGCAGGAACCT
 TCGCGTTGGTGGGAGCTTGGCATACTTCCGGCAGTGGATATGGTCCGCACTGGGATGGTGTGAC
 CTGAAGATGGCAATGGTCACTGCATTCCGATGGTCTGGTATCGGACCTATCAACTGAAAGTGGCATGACGATGAC
 GGTGCTCTCTTGGCATGATGTTGTCGACTCTGGTTCAAGTTAGCCAGATATATCGACAGCACGATACTGATGCTT
 TCTATGGTTCGGGATCACACATCTTCACTCAACCCAGTCATGGGCTGAATACGGCTACTCAAGATGCGATCTGAAC
 TTGTTATGGGTTCTATGTTATTGTTACCAACTACTGTGGATGACAGGATGGCTGGTCCGAATTCAAGCAGGGTC
 TGTTCTGAACGGATTGAGCAGAGGGACTGAAGGAGTTCAAGCCGCCAGGAAGAACAGGAAATAGAGTTAAAACGCAG
 TTTGA

>ORF9005c (SEQ ID NO:68)

GTCAGCCCACCACTGCTTGCAGGTGGTAGCCGCCACCCGCCACCTGAGGCAGGCCGATCGGGGTGGCGTTGT
 AGGGCCACGACTGACGGGACTCTCGAGTAGTCGGTGTGTTGACCTCCGGGTTGTTCAACAAGAATGGGAGGCCGATC
 CAGTTCAGGTCTGCAACGCCCTGTTGTCCTGGCGACGGAGGCCAGGTGGGTTGCCGATGAAACAGCCGCCACGGGA
 AGGCCGCTAGCAGTCTGGAAAAATCAGCGATTCTTGCCAGCAGCGGATTGTTACGCCGTTGCGTGTGTCACCTCCA
 TTGCGATCTGCCGAGATCCGTGCCGACGGAAATGGCCGCGATGCCGCGCTGGTGAAGCCCTGGACAGGGCGTGCATC
 ATCGCCACCAAGAGGCCATCTGCCACTCTGCCGCCAGGCTGCTGAAGGAGCTGACCGCCGGTGTCCGCCGGTGC
 CGGAGATTGATTGGCACTGCTGGCGCAGTCTGGTCAACTCGATGGTGTGAAAGCTCACGTTGACGACCGGGATCC
 CCGCCAGGGCACCACGATGAGCCGACGTTAGATGCGTCTCGATGCCGAGAGACAGCACTCCCTGTTGCCCTCG
 TCGGCCTTCCCACGAACTTCAGCCATTGCCGATCACGATGCCGCAACGGCACCGCAACAGGCCAGTATCCGA
 GATCATGTCAGATCCGTTGTTGATGATCAAGCCGAGGAGGGTGAGGTAATACTCCAGGTAGTCATTGGTCA
 TCATGCTGCCCTCCGTGCCAGTAG

>ORF8222 (SEQ ID NO:70)

CTACCTGGAGTATTACCTCACCCCTCGGCTGGATCATCAACACGGGATCTGAAACATGATCTGGATACTGGCCTGT
 TCGCGGTGCCGTTGCCGATCGATGCCGAAATGGCTGAAAGTTGTTGGGAAAGGCCGACGAGGGCAACAAGGGAA
 GTGCTGTCCTGCCGATCGAGACGCATATCTACGTCGGTACATCGGGCTGCCCTGGGGGATCCGGTGTCAA
 CGTGAGCTCGACACCATCGAGTCGACCAAGACTCGGCCAGCAGTGGCAATACAATCTGCCGACCGGCCGACACCG
 GCTGGTCGAGCTCTTCAGCAGCCTGGCGGAAGAGTGGCAGATGCCGCTGGTGGGCGATGATGCAACGCCCTGTCC
 AAGGGCTTCAACCAGCGGCCATCGGCCATTCCGTGCCAGGATCTGCCAGATGCGAATGGAAGTGGACAACAC
 GCGCGTGAACAATCCGTCGTCGACAAGAAATCGCTGA

>ORF8755c (SEQ ID NO:72)

CAGTCTGGAAAATCAGCGATTCTTGTGCCAGCAGCGGATTGTTCACGCCGTGTTGTCACCTCCATTGCACTG
 CGCGAGATCCGTGCCACGGAATGGCCGCGATGCCGCGCTGGTGAAGCCCTGGACAGGGCGTGCATCATGCCACC
 AGAGCGGATCTGCCACTCTGCCGCCAGGCTGCTGAAGGAGCTGCCAGGCCGCTGGTGGGCGATGATGCAACGCCCTGTCC
 TATTGGCACTGCTGGCGCGAGTCTGGTCAACTCGATGGTGTGAAAGCTCACGTTGACGACCGGGATCCCCGCCAGGGC
 GACCAACGATGTAG

>ORF9431c (SEQ ID NO:74)

CTGAAACCAGAAGTCGACGAACATCATCGCAAAGAAGACGACCGTCATCGTCATGGCAACTTCAGTTGATAGGTGCCGA
 TGACCAGGACCATCGGAATGCAGATGACCATTGCCATCTCAGGAACGACATCACCATCGGCAGTGCCTGGCGGACCATA
 TCCATCGCCGGGAAGTATGCCAAGCTGCCACCGAACGCCAGGGTCTCGCGATGCCGTTACCGGTACCGTGGCTGGAGGGTGA

>ORF9158 (SEQ ID NO:76)

CGTCTACACCGATTACGGCGGGCAGGTGGCGGCACCGTGTGGAACGGCATCGCGAGAACCGCAGGAACCTCGCGTTG
 CGGTGGGAGCTTGGCATACTTCCGGCAGTGGATATGGTCCGCCAGGCAGTGCCTGGTATGTCGTTCTGAAGATG
 GCAATGGTCATCTGCATTCCGATGGTCTGGCATCGGCACCTATCAACTGAAAGTGCATGACGATGACGGTCGTCTT
 CTTTGCATGATGTTCGCAGTTCTGGTTAGTTAGCCAGATATCGACAGCACGATACTTGA

>ORF10125c (SEQ ID NO:78)

GTGATAGCAGGATGCCTCCCTTGGGAGCCAGGAGATTGATGATGAAACGCGCACACCAACAAAGGCTTGCCCTCCGGAT
 CGGTTTGGTCTGGGTATGCTTGTGCGTTCTGCCTGCATGATGCCGTCAGCTACGTTGGGTAAGCGAGTTAGCC
 TATTCTTGTAGTAGCTCTTGTAGTGTACAGAAATTATGTGGCTTGGGGTATCAATGACTCTACTGTGTGCTTT
 CTGGTGGGATTTGCCTGGTTAAAGGGGACATCTCGTCTAAAGGGTCTCCAAGTCGAGATGTCCTCAACTATGACTTC
 ACAAGCTGAAACTGAATCTGTAGCAGAGCTGTTGACTATCAGGCAGCACACCATTACGGGACTAG

>ORF9770 (SEQ ID NO:80)

TCAAAACAGCTCTGCTACAGATTCAAGTCAGTTCAGCTTGTGAAGTCATAGTTGAGACATCTGACTTGGAGACCCTTAGAGAC
 GGAGATGTCCTTAACCAAGGCAAATCCCACCAAGAAAGACACACAGTAGAGTCATTGATACCCAGCAAGCCACATAA
 AATTCTGTGACACTACAAGAGCTACTAACAAAGAATAGGCTAACGCTTAACCCAAACGTAGAGCTGGACGGCAGTCATGC
 AGGCAGAAACGCACAAGCATAACCCAGACCAAAACGATCCGGAGGCAAAGCCTTGTGGTGTGCGCTCATCATCAA
 TCTCTGGTCTCCAAAGGGAGGCATCTGCTATCACCTATACGCCAAAAGATGATTGGCAAGCATTATGGCATATTAA
 TGCCCACTAGCTATCTGCCACTGGAGTACCTCATGGCAACCGAAACGCTGCTCTCCGATCCGCTGGAGCAGGATATC
 AACAGAGCTGGTGGAGACCGGCCGCTATCAGAAATCGCAGCGAAGTCATCCGGCAGGCTTGCCTGCTGCAACAGGA
 AGCCCAGATANGCGCCAAGCTCGAAACCCCTCCGCAACGCAACATCCAGTGGGCTGATGCAACTGGAGCGCCGAGTACG
 ACGAGATCACCAGCGACGAACGGCCAATACCTGACGAGCTGGCAACCAGGGAGCCACTGA

>ORF9991 (SEQ ID NO:82)

AGCTGGACGGCGATCATGCAGGCAGAAACGCACAAGCATAACCGACACAAACCGATCCGGAGGCAAAGCCTTGTGG
 TGTGCGCTTCATCATCAATCTCTGGCTCCAAAGGGAGGCATCCTGCTATCACCTATACGCCAAAAGATGATTGG
 CAAGCATTATGGCATATTATGCCACTAGCTATCTGCCACTGGAGTACCTCATGGCAACCGAAACGCTGCTCTCCGA
 TCCGCTGGAGCAGGATATCAACGAGCTGGTGGAGACCGGCCGCTATCAGAAATCGCAGCGAAGTCATCCGGCAGGCTTGC
 GCCTGCTGCTGCAACAGGAAGCCCAGATANGCGCCAAGCTCGAAACCCCTCCGCAACGCAACATCCAGTGGGCTGATGCAA
 CTGGAGCGCCGGCGAGTACGACGAGATCACCGAGCAACTGGCCAATACCTGACGAGCTGGCAACCAGGGAGCCA
 CTGAAGCATGGCCAAGTACCGCATCTCATGA

>ORF10765c (SEQ ID NO:84)

CACCTGGCTGTGCCACCCGGTAGAAGACGAAGTGCCTGGGCCAACAAACCTTACCGACATTGGGATCGAGTGGCAGT
 AAACGAGGTGGATGCTGCGAGGCCAGCTCCAGTTCTCAGGCTGATGCTGCCACCTGTTGTGGGTCTGTCGCAACT
 GCTTCCAGCGCCGCCCTATGAGTGCCTGGTAACGTCGGCGCGGCATGCCGAAGTGGTTGTGGGTGAAGCGCAGGAT
 ATCGACGATGTCCGTTGGCATCATGAGAGATGCGGTACTTGGCCATGCTTCAGTGGCTGCCCTGGTGCAGCTCGT
 CGAGGTATTGGGCCAGTTCGTCGCTGGTATCTCGTCGACTCGCCGCGCTCCAGTTGCATCAGCCCACGGATGTTGCG
 TTGCGGAGGGTTCTGAGCTTGGCCNTATCTGGCTTCTGTCAGCAGCAGGCCAGCTGCCGGATGACTTCGCT
 GCGATTCTGATAGCGGCCGGTCTCCACCAAGCTCGTTGATATCCTGCTCCAGCGGATGGGAAGGACGACGTTCGCGTGT
 CCATGAGGTACTCCAGTCGGCAGATAGCTAG

Fig. 3-10

>ORF10475 (SEQ ID NO:86)

AGCATGGCCAAGTACCGATCTCTCATGATGCCAAGCGGACATCGTCGATATCTGCGCTCACCCACAACCCACTTCGG
CGATGCCGCGCCGACGTTACCAGGCACTCATAGGGCGCGCTGGAAAGCAGTTCGACAGACCCACAACAGGTAGGCA
GCATCAGCGTGAAGAACTGGGAGCTGGCCTGGCAGCATCCACCTCGTTACTGCCACTCGATGCCAATGTCGGTAAG
GTTGTTGGCCCCAGGCACCTCGTCTTCTACCGGGTGGCAGACAGACCAGGTGCTAGAGGTGGTTCGCGTGCCTCACGACGC
CATGGATGTGGATCAACACCTGCCCAACGATGA

>ORF11095c (SEQ ID NO:88)

AGCCGCATGCAAGCGTGGTCAGCACGAATGCAAATGCTGGTCAGGGGGATGCAATCGAGTGGTCAGGCCACTGCTAT
TGCATCAACCATGGGCACCTGCTGGATGTTACCCGTAGCCTTCTGTTGCCGGCGAACGCAGCCCTT
CTGCCTTCCGGCAGGCCCTTCGGTAGGGCTTTACCCCTGTGAACCATTCCCTCGCCCTCAAGCCCATTCCCCCTT
TGGGCCATTGCTCTGTTACAGTTGCTCATCGTGGGCAGGTGTTGATCCACATCCATGGCGTCGTGAAGGCACGCGAA
CCACCTCTAG

>ORF11264 (SEQ ID NO:90)

ACCGCGGTGCGGAGAGATCTCTCAAACGTGGTTGCACGCATATCGAAGCAGATTACATAGGAGGCTTGCCTGTT
AACAGCTCCTGAGGGACTTGGTTGCCATGGTTCCACGGCCAAATCGTGACGTATTGACGATTCCGCTGGCTTT
TCAGTACGCATCGCTGGCGCTCATTACCCAGCCAAATGCGGCCTTGCCTGACCAAGCGATTCCAAGGACTGCGATC
CATGTAGCCAGCCCTAATGCATGTATGTATAGGTAAAGTCGTCGTATTCGGCTGGATGTGCTGA

>ORF11738 (SEQ ID NO:92)

GAAGAGGTGATCATGAAGTACAGGCATATCGGCTGCAGAACTACCGCCGGCTGCGCATGTTGTATCGAGCTCGATGA
CGAAATTCTATCTTGTGGTCCAACAACAGCGGAAGACATCCGGCGTCAAGGCGTGTACTCAATGCTCGGGCG
AACTGAAGAAGTTCGAGCTTTGACTTCAGTGCAGCGCTGTGGGCCAGAGATCGATGCGGTGCCAGGACGCCCTGG
GATGAGGAATGCGCCAAAAGGTACCGTCCATACTCTTGATCTCTGGTTCGGCTCGGTGAAGACGACCTCGGCACTGC
GATGTCGCTGCTGCCAGCACTGAGTGGGACGGCAAGTGCCTGGGATCCGGGTAGCCTCGAGCCTCGGGATGCCACG
AGCTCGTCTGGAAGTCCATGAACATGAGAAGGCCAACACGCACTGTCGCCCTGGGCCAGCGCAAGGCCGCC
GGGGAGCAAGCTGTGGAGGGGGCGCGGAAGACGGCTGCGGTGGTGGCCATGCCGGCGAGTACAAGCCTGGCCAGA
AAGCCTGACGAAGTACCTCACAAAGGAACGTAGCAAGGAATACACCTCCGCTACTACGTGCTCGATGAGGGCTTTG
TCGGCTATCAGGCAAGGGAGGCCACTACGAGCCGCTACCCCTAGGCAAGGAGCCGGCGGTGAGCCATTCTCAAGTCG
CTGGTGGGTGCACTCCTGCGCGCAGGGCACCTCGATGACCCAGATGCCGGTAGCTGATCGCGCAGAGAGCTT
GTCGCGCGCTGAGCAGGTCTACCGCAACCTGGAGAAGCGTGGCAGCACCAGTCGGCTCTCAAGGGCTAGATA
CCTCGGAGAAGGAGCTGAACTTCCACCTGAAGGAAGTCTCAATGACACCCCTCACGCCCTGGCAAGCTGGCTATCCG
GGCGTCAACAATCCGGAGATCGTGAATTGGGGGGCTTGGATCCGACCACTGCTTGGGGCAAGACGCCAGGTTCACTA
CGTGAATCCGGGCGTAGCTTCCGCCACTGCCAGACAGCTACAATGCCCTGGGGTCAAGAACTGGTCTACATGGTGG
TTGAGCTGCTGACTTGCACGAGCAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGTTCACTAGGAACGTTTGCCTCCTTGG
CCTGAGGCCATCTGACCGCAGATCCAGCAGGTCTTCACTAGGAACGTTTGCCTCCTTGGAGGATGCTAACGATCA
CGCAGCTTGTTCACACGCACTCGTCACTACCACGCACTCCCCCACATCTCATGAAACCGGATTCTGCCATT
GGTACTTCCGCCGCTCAACGACCAAGTGGGCCATCACCGATGTGCCAATCTGCTATTCAAAACGGGCGCTCC
GACGCTCCAGCGCGCAATTCTGAGCGGTATCTGAAGCTGACGCACTGCGATCTCTTCCGACGCCGTGATATT
GGTGGAAAGGCAACGTCGAGCGTCTGCTCTGCCATGGTCCAGGAGCTGATGCCCTTGGCTCACAAACACTGGTCACT
ACGGATCTGGACAGCGTGACGGTAAGACGGAGCCGAGAAGGCCGCCGCAAGGCCAGGGCGCTGAGGGCGCCGTTGA
CGGAGATGACGAGGACGAGGACGACCTGAAGCCCTCGAGCTGAAGACGACGAGAAGCAGAACCGAGTGGCAAGA
AGAAAGTCCAAGAAGCGTGGCAGCACCTGCCATGCACACGTTGGAGGTGCCGTACGTCACCAACCCATCAGCTGG
ATCCCCGAAGAAGCGGTGATGGCAGAGCTTGGGAAGTCACGGCGGAGCAAAAGACGCTGTCGCTGGCTGAGGATTCCAG
CGCTGGGGTCTGGTAGCTTACAGACCAAGGTTTGGTACGGTGGTGCAGCAGACATCACAGCTCTGCGCCGACAC
TTGAGGAGGCCTTGGTCTTGAGAACGCGGACTGGTGCAGGCTGAGGCAAACCGGTGGCTCAAGCTCAAGGCC
GCACCGAGCAGCCCTGAAGAGCTGGCTGAGAAGTTACACGATAGGGTGGTGGCAAGAACCTCGACAAGACCCGCTTGC
GCTGGAGGTACTCGCAAGCGGGCGCTAATGGCTGGAAAGGTTCCCGCTACATGCCGAGGGCTTGGCTGGCTGAAAG
CCAAAGTGGCCACGAGCTTGGAGGCGATGCTGCCATGCCACCGAGGTGCGACTATTGAGGCCACTACAGCCGATGTT
GTCGCTATCATTGTTGACCCGGGGCAGACGGCATGA

Fig. 3-11

>ORF12348c (SEQ ID NO:94)

CGGAAGGTGATTCCCTGCTCAGTCCCTTGTGAGGTACTTCGTCAAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATIC
 GGCCACCAACCGCAGCCGCTTCCCGCAGCCCTCACAGCTGCTCCCGGCCCTGGCGCTTGGCCGAAGCGCGA
 CAGCTGCGTTGGCCTCTCATGTAGTTCATGGAACCTCCAGACGAGCTCGTGGCATCCCGAGGCTCGAACGCTACC
 CGGATCCCACGCACTGCCGTCCACTCGTCTGGCAGCAGCAGCACATCGCAGTGGCAGGTCCTACCGACGCG
 GAACACAGAGATCCAAGAGTATGGACGGAACCTTTGGCGCATCCTCATGCCAGGGGGCTCTGCCGACCGCATCGA
 TCTCGGCCACAGCGCCGACTGAAGTCAAAGAGCTGAACCTCTCATTCGCCGAAGCATTGAGTACAGGCTTGG
 ACGGCGGATGTCTTCCCGTGTGGCACCGACAAAGATAGAAATTGTCATCGAGCTGATGACAACATCGCGCAG
 CGGGCGGTAG

>ORF12314c (SEQ ID NO:96)

GGTACTTCGTCAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATGCCACCGCAGCCCGTCTCCGCCGCCCCGCC
 TCCACAGCTTGTCCCCGGCGGCCCTGGCGCTTGGCGCAAGCGCAGCAGCTGCGTTGGCCTCTCATGTAGTTCATG
 GAACTTCCAGACGAGCTGTTGGCATCCCGAGGCTCGAACGCTACCCGATCCGACGCACTGCCGTCCACTCAGTGC
 TCGGCAGCAGCAGCACATCGCAGTGGCAGGTCGCTTCACCGACGCCAACAGAGATCCAAGAGTATGGACGGTAACCTT
 TTGGCGCATCCTCATGCCAGGGGGCTCTGCCACCGCATCGATCTGGCCCACAGCGCCGACTGA

>ORF13156c (SEQ ID NO:98)

CGACAGATTGCGCACATCCGTGTGATGGCCAACGGTGTGACGCCAGGCGGAAGTACCGAATGGCGAGAATCCGCGTT
 CATAGAGGATGTGCGGGGAGTGCCTGGTGTGACGAGCTGCGTGTGAAACAAAGTCGCGTGTGATCGTTCAGGATCCTCAAGG
 AGGCGCAAAACGTTCTGATGAAGACCTGCTGGATCTGCGCGTGCAGATGCGCCTCAGGCTCTCAATGAAGACCAAATG
 AAGCGGAGCTGCTTGTCACTCCTCGCTTCACTGCTCGTCAAGTCGAGCAGCTCAACCACCATGTAGACCAGATTCT
 TGAACCCCAGGCCATTGTAGCTGCTGGCAGTGGCGGAAGCTACGCCGGATCACGTAGTGAACCTTGGCGTCTTGC
 CCCAAGACAGTGGTCGGATCCAAGGCCGCCGAATCACGATCTCCGGATTGTTGACGCCGGATAGCCGAGCTTGGCCAG
 GCGCGTGGGTGTATTGAAGACTTCCCTCAGGTGGAAGTTCAGCTCCTCTCCGAGGTATCTAG

>ORF12795 (SEQ ID NO:100)

CTTCCGCCAACTGCCAGACAGCTACAATGGCCTGGGTTCAAGAATCTGGTCTACATGGTGGTTGAGCTGCTCGACTTG
 CACGAGCAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGCTCATGGTCTTCATTGAGGAGCCTGAGGCGCATCTGCA
 CGCGCAGATCCAGCAGGTCTCATCAGGAACGTTTGGCGCTCTGAGGATGCTAACGATCACCGACTTGTCCACA
 CGCAGCTCGTCACTACCACGCACTCCCGCACATCCTCATGAAACGCCATTCTGGTACTTCCGCCGCGTC
 AACGACCAGTTGGGCCATCACACGGATGTGCGCAATCTGCGTATTCAAACGGCGTCCACGCTCCAGCGCGCA
 ATTCCCTGAGCGGTATCTGA

>ORF12314c (SEQ ID NO:96)

GGTACTTCGTCAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATGCCACCGCAGCCCGTCTCCGCCGCCCCGCC
 TCCACAGCTTGTCCCCGGCGGCCCTGGCGCTTGGCGCAAGCGCAGCAGCTGCGTTGGCCTCTCATGTAGTTCATG
 GAACTTCCAGACGAGCTGTTGGCATCCCGAGGCTCGAACGCTACCCGATCCGACGCACTGCCGTCCACTCAGTGC
 TCGGCAGCAGCAGCACATCGCAGTGGCAGGTCGCTTCACCGACGCCAACAGAGATCCAAGAGTATGGACGGTAACCTT
 TTGGCGCATCCTCATGCCAGGGGGCTCTGCCACCGCATCGATCTGGCCCACAGCGCCGACTGA

>ORF13156c (SEQ ID NO:98)

CGACAGATTGCGCACATCCGTGTGATGGCCAACGGTGTGACGCCAGGCGGAAGTACCGAATGGCGAGAATCCGCGTT
 CATAGAGGATGTGCGGGGAGTGCCTGGTGTGACGAGCTGCGTGTGAAACAAAGTCGCGTGTGATCGTTCAGGATCCTCAAGG
 AGGCGCAAAACGTTCTGATGAAGACCTGCTGGATCTGCGCGTGCAGATGCGCCTCAGGCTCTCAATGAAGACCAAATG
 AAGCGGAGCTGCTTGTCACTCCTCGCTTCACTGCTCGTCAAGTCGAGCAGCTCAACCACCATGTAGACCAGATTCT
 TGAACCCCAGGCCATTGTAGCTGCTGGCAGTGGCGGAAGCTACGCCGGATCACGTAGTGAACCTTGGCGTCTTGC
 CCCAAGACAGTGGTCGGATCCAAGGCCGCCGAATCACGATCTCCGGATTGTTGACGCCGGATAGCCGAGCTTGGCCAG
 GCGCGTGGGTGTATTGAAGACTTCCCTCAGGTGGAAGTTCAGCTCCTCTCCGAGGTATCTAG

>ORF12795 (SEQ ID NO:100)

CTTCGCCAACTGCCAGACAGCTAACATGGCTGGGTTCAAGAACATGGCTACATGGTGGTGGCTGCTGACTTG
 CACGAGCAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGCTTCAATTGGCTTCATTGAGGAGCCTGAGGCCATCTGCA
 CGCGCAGATCCAGCAGGTCTTCATCAGGAACGTTGCGCCTCCTGAGGATGCTAACGATCACGCCACTTGTCCACA
 CGCAGCTCGTACATCACCACGCACTCCCGCACATCCTCTATGAACGCGGATTCTGCCATTGGTACTTCCGCCGCGTC
 AACGACCAGTGGGCCATCACACGGATGTGCGCAATCTGCGTATTCAAAACGGCGCCTGGACGCTCCAGCGCGCA
 ATTCCCTGAGCGGTATCTGA

>ORF13755c (SEQ ID NO:210)

GCTACCCGAACCCAGCGCTGGAATCCTCAGCCAGCGACAGCGTCTTGTCCGCCGTGACTTCCCAGAGCTCTGCCAT
 CGACCGCTTCTCGGGATCCAGCTGATGAGGGTTGGTGGACGTGACGGCACCTCCACGTGTCATGGCAGGTGCTGC
 CACGCTTCTGGACTTCTTCTGCACTCGGTCTGCTCGTCGTCCTCAAGCTCGAAGGGCTTCAGGTCGTCGTC
 TCGTCTCGTCATCTCGTCAACGGCCTCAGCGCTGCCCTTGCAGGGCCCTTCTGGCGTCCGTCCTGACCGT
 CACGCTGTCCAGATCCGTGATGACCAAGTGTGAGGCCAACGAGGGGATCAGCTCTGGAAACCGATGCCGAACGCAC
 CACCGACTCAAGGATGGTAGGGCGGAAGAACGCAAGGCGCTGGCCACCAACTCGATCATTGCAAGGAGCAGACGC
 TCGACGTTGCCCTCCACCAATATCACCGCTCGGAAAAAAAGAGATCGCAGTGCCTGAGCTCAGATACCGCTGCAGGA
 TCGCGCGCTGGAGCGTGGACGCCGTTGAAATAGCGACAGATTGCGCACATCCGTGTGA

>ORF13795c (SEQ ID NO:212)

TGTCTCGCACCCACCGTACCGAACCTTGGCTGGTAAGCTACCGAACCCAGCGCTGGATCCTCAGCCAGCGACA
 GCGTCTTTGCTCCGCCGTGACTTCCCAGAGCTCTGCCATCGACCGCTTCTCGGGATCCAGCTGATGAGGGTTGGTGTG
 GACGTGACGGCACCTCCACGTGTCATGGCAGGTGCTGCCACGCTCTGGACTTCTTGTCCACTCGGTCTGCTC
 GTCGTCGTCCTCAAGCTCGAAGGGCTCAGGTCGTCGTCCTCGTCATCTCGTCAACGGCCTCAGGCCCTG
 CGCCTGCGCGGCCCTCTCGGCGTCCGTCTGACCGTCAGGCTGTCAGATCGTGTGATGACCGAGTGTGAGGCCA
 ACGAAGGGGATCAGCTCTGGAAACCGATGCGCGAACGCAACGACCGACTCAAGGATGGTTAG

>ORF14727c (SEQ ID NO:214)

CAGGAAGTCGGCAGCTGAAGGATGCTCTCGTGGCCAAGTATGCCCTGGCTAGTCAGGCCACGCCGTAGTTGAACG
 CCTGACGCCGCCACGCCCTCCAGGCTTCGGACATATCGCTCTGGCTGGCCTTGTCTGCGCGTGGCTGCCGG
 ACACCGAGCTGTAATTCTCGAACCTTCTCAAGTTCGAGATCCGCTGCCGATGTCGTTCTGAGCCAAACCTGAT
 GTCGGCTGGAACGTTGCAATAGACCAAGTAAAGCTGGATGGTCAGACATGAACAGCGGGTCATCGTTGACGT
 CCGCCAGGATTTCTGGTGGCAAGGTCGGTACGTGATGACGCACTATCTGCTCCTGCCCGCATGCTGGCGCC
 TGCTCCGAGATCACCAGTCAGGCCCTGATGAGGGAGGTGGTCTGCGGAAACCTGCGCCAGCACGAACCAACGAAGGG
 CTGCGGAGGGTCGCTACAATGCACTGGCTGGATCTCGGCTGGCTGGTATCTGGCTATAATTGCTGCTCATGC
 CGTCTGCCCGGGTCAACAATGATAGCGACAACATCGGCTGTAGTCGGCTCAATAGTCGCACTCGGTGGCAGTGGCAG
 CATCCGCTCAAGCTCGTGGCCACTTGGCTCGAGCCAGGCCAAGCCCTGGCGATGTCAGGGAAACCTCCAGCCA
 TTGAGCGGCCGCTTGGCGAGTACCTCCAGCGCAAAGCGGGCTTGTGAGTTCTGCGCACCCCTACGTGTAACCT
 CTCAGCCAGCTCTCAGGGCTGCTCGGTGGCGCTTGAGGTTGAGGCCACCGGTTGCCAGCCTGGCACCA
 CGCGTTCTCAAGACCAAGGCCCTCAAGTGTGCGGCCAGAGCTGTGATGTCGCACTCGTACCGAACACC
 TTGGTCTGGTAA

>ORF13779 (SEQ ID NO:216)

CGGTGGGTGCGACGACATCACAGCTCTGCCGCCACACTTGAGGAGGCCCTTGGCTTGAGAACGCGGACTGGTGCAG
 GCTGAGGCAAACCGGTCGGTGGCTGCCCTCAAGCTCAAGCGCGCACCGAGCAGCCCTGAAGAGCTGGCTGAGAACG
 TAGGGTGGTCGGCAAGAACCTCGACAAGACCCGCTTGGCTGGAGGTTACTCGCAAGCGGGCCGCTCAATGGCTGGAGG
 TTCCCGCTACATCGCCGAGGGCTTGGCTGGCTGAGGCCAACGAGCTTGAGGCCAGTGTGCTGCCATGCC
 ACCGAGGTGCGACTATTGAGCCGACTACAGCGATGTTGCGTATCATTGTTGACCCGGGAGACGGCATGAGCAGA
 CGAATTGA

>ORF14293c (SEQ ID NO:218)

GGGAGGTGGTCTGCCGGAACCTGCGCCAGCACGAACCACGAAGGGCTGCGGAGGCCTCGCTACAATGCATGCGTGGATC
 TCGCGGTGCGCGTCGGTATCTGGGCTATCAATTCTGCTGCTATGCCGCTGCCCGGGTCAACAATGATAGCGACAACA
 TCGGCTGTAGTCGGCTCAATAGTCGCGACCTCGGTGGCGATGGCAGCATCCGCTCAAGCTCGTGGGCCACTTGGCTTC
 GAGCCAGGCCAAGCCCTCGCGATGTACGCGGAACCTCCAGCCATTGAGCGGCCGCTTGCAGTACCTCCAGCGCAA
 AGCGGGTCTTGTGAGATTCTTGCACGCCACCCCTATCGTGTAA

>ORF14155 (SEQ ID NO:220)

CCCGGGGGCAGACGGCATGAGCAGACGAATTGATAGCCCAGATAACGACGCCGACCGCAGATCCACGCATGCATTGTAGC
 GACGCCTCCGCAAGCCCTCGTGGTTCTGCTGGCGCAGGGTCCGCAAGACCACCTCCCTCATCAAGGCGCTGGACTGGG
 TGATCTGGAGCACGGGCCAGCATGCGGGCAGGAAGCAGATACTGCGTGCATCACGTATAACCGACCTTGCCACCAAT
 GAAATCTGGCGGACGTCAACGATGACCCGCTGGTTCATGCTCGACCATCCACAGCTTTACTGGTCTATTGCAAAGAC
 GTTCCAGGCCAGCATCAAGGTTGGCTGAGAACGACATCCGCAAGGCCATCTCCAACTTGAAGAAGAGTTCGAGAATT
 ACAGCTCGGTGTCGGCAGACCAAGCGCAGAGGAACAAGGCCACCAAGGCCGATATGTCGAAGGCTGGACTCCGAGGCTGTG
 GCCGGCGTCAGGACGTCAACTACGGCGTGGCGACTACGCCAAGGGCATACTTGGCCACGAGGACATCCTTCAGCT
 CGCCGACTTCTGCTACAAAACCQCCCGCTTGTCCGACGGGCTGCGCTGAGCTACCGCTGTTATCGATGAGA
 GTCAAGGACACGTTCCGGGTGAGTGAAGTCTTCAGGAAGTGGAAAGCCAGATGCAGGGCAAGTTCTGCTTGGTTTT
 TTGGCGACCCGATGCACTGATCTTCATGAGAGGCGCAGGGGACATCCAGCTGAGGATCATTGGCGGCCATCACGAA
 GCCGGAGAACTTCGCTGCGCAAGCAGATCCTGACGTCGCAATGCCGTGCGCGCAGGGCAGGGCATGGATGGCTGGAGAAG
 TCCGCGGGCTGACGAGAGGGTCAAGGAAACCTCAAGCTGGAGGGGTCGGCCGGATGTTGCTTGGCGACACAG
 CTGAACCGAACCGAGGCTTGGCAAGAGTCCGAGCGTGGAGCTCGGCACGAACAACGACGAGGGTTGGACAACCCAGA
 CATCGCAGTCAGATTCTGTCATCGTCACCGCATGGCCCAAACCCGCTGGCTTGGCGCATCTACTCGGCGCTGA
 ACGACAAGACGTCGGATGCCATGAAGCAAGGGATGCAGGACGGCACGGGTTGGCCGTTGACCCCTCTAAGTTTGC
 CTACCGATCGTGCAGCTGTAAGGCCGCAATGAGTCGGCGATGAGCCTGCTCCGGGAATTCAAGCCGCGCTGG
 GCCTGCGGCTCTGACCCGCCAGCTGCGCGATGTTGCGAGAGCTGACGCTGCTGCGTCAGGCTTGTGCGCATGC
 TGGACGAGGCAGGGACCACTGGTACATAGCTCTCATCTGTGACACGGGCTTTTGAGTTGACGAGGCTAT
 GCGCGTGTCTGGGTTTGTCAAGGATATTGTCACCCCTCAGGAGGCCAGGTGCTGAGTCAGITCCGGCGAAGG
 ATTATCCTGGACCGACAATGCCAAGTTCTCAATTGCTCTGCGCAAGAGCTTGGCCATGAAACGCTATGTCAG
 AAGGCTCCCCCTATGCCACCGCAGCACGGCGTAAGGGAGCGCAGTTGCAACGCGTATGGTGGATGGACGAGGAAGAA
 AGCGACTACCGAACGTACAACACTACGAGCGTGTCTCGCGAGTGCTGAGGCCGCGCTGAGATCGTCACGAGCACTAGA
 CGGTGATGAAAACACTGGAGCCGAACGCTGCACTGCTTACGCTGCACTCGTGGCCAGCAGGGGCTGGTACTAG
 CGTTCTTGTGCGCACCCCTGCGACCCCTGGAAAACGTCGTGGCAGCAGGGATCTGCGCGAAGCGCAGTCTTACG
 CAGGAAGTGTAGTTGGATGGCCATAG

>ORF14360 (SEQ ID NO:222)

TCGCGTGCATCACGTATACCGACCTTGCACCAATGAAATCTGGCGACGTCAACGATGACCCGCTGGTTCATGTC
 ACCATCCACAGCTTTACTGGTCTATTGCAAAGACGTTCCAGGCCACATCAAGGTTGGCTGAGAACGACATCCGCA
 GCGGATCTCGAACCTGAGAAGAGTTGAGAATTACAGCTCGGTGTCGGCAGACCACGCCGACAGGAACAAGGCC
 ACCAAGAGCGATATGTCGAAGCCTGGAGGCTGTCGGCGCTCAGGACGTTCAACTACGGCGTGGCAGTGA
 CTACGCCATACTTGGCACGAGGACATCCTGACGTCGCCACTTCTGCTACAAAACGCCGCTTCCGACGGGCGT
 GCGCGCTGA

>ORF15342c (SEQ ID NO:224)

GAAGGGTCAACGGGCAACGGTGGCGCTGATCCCTGCTTCAAGGATCCGACGTCCTGCTGAGCGCCGAGT
 AGATGCCGCCAGCCAAGCCAGCGGTTGCGGCCATGCGGTGACGATGACAAGAATCTGACTGCGATGTCTGGGTTGTC
 CAACCCCTCGTGTGTCGCGCAGCTCCACGCTCGGACTCTTGCAAAGCCTGGTTCGGTTCAAGCGTGTGCGCA
 GACGAACATCCGGGCCACCCCTCCACCGCTTGAAGGTTCCATGACCCCTCTGTCAGGCCGAGCTTGCTCCATGC
 CATCGCCCTGCGCGCAGCGCATTGGCAGCTCAAGGATCTGCTTGGCGAGCGAAAGTTCCGGCTTGTGATGGCC
 CGCCAATGATCTCAAGCTGGATGTCCTGCGCTCTCATGAAGATCGACTGCATCGGGTCCGCAAAAACCAAGGCA
 GAACTTGGCTGATCTGGCTTCACTTGAAGACTTCACTACACCCGGGAACGTCGTCTGACTCTCATCGATAA
 ACACGAACGGTAGCTCAGGCCACGACCCGCGGAACAGCGGGGGTTGTAG

Fig. 3-14

>ORF15260c (SEQ ID NO:226)

ATGCCGCCGAAGCCAAGCCGGTTGCGGCCATGCGGTGCACGATGACAAGAATCTGACTGCGATGTCTGGGTTGTCCA
 ACCCTCGTCGTTGTCGCGAGCTCCACGCTCGGACTCTTGCCTAAGCCTCGGTTCGGTCAGCGTGTTCGGCAAGA
 CGAACATCCGGGCCACCCCTCACCAGCTTGAGGTTCCCATCGACCCCTCTCGTCAGCCCCGCGACTTGTCCATGCCA
 TCGCCCTGCGCGCAGGCATTGGCGACGTCAAGGATCTGCTTGGCGAGCGAAAGTTCTCCGGCTCGTATGGCCCG
 CCAATGAA

>ORF14991 (SEQ ID NO:228)

CGTCGCCAATGCCGTGCGCGCAGGGCGATGGCATGGAGCAAGTCCGCGGGCTGCACGAGAGGGTCGATGGAACCTCA
 AGCTGGTGGAGGGTCGGCCCGATGTTCGTCTGCCAACACGCTGAACCGAACCGAGGCTTGGCAAGAGTCCGAGCG
 TGGAGCTCGCGACGAACAAACGACGAGGGTTGGACAACCCCAGACATCGCAGTCAAGATTCTTGTATCGTCACCGCAT
 GGCGCAAACCGGCTGGCTCGCGCATCTACTCGGCCTGAAACGACAAGACGTCGGATGCCATGAAGCAAGGGATGC
 AGGACGGCACCGGTTGGCCGTTGACCCCTCTAAGTTTGCCTACCGATCGTGCAGCTGTGAAGGCCGGCAATGAA

>ORF15590c (SEQ ID NO:230)

CGCTCGTCAACTAAAAAGACCCGTGTACAGAGATGGAGAGCTATGTCACCAATGGTGGTCCCTGCCTCGTCCAGCAT
 GGCGACAAGCCTCGACCGCAGCGCTCGCAATACATCCCGGGCACGTCGGCCGGTCAAGAGCCGAGGCCA
 GGCGCGGGCTGAATTCCGGAGCAGGCTCATCGCCGCAACTCATTGCCGGCCTTCACAGCTGCAACGATGGTAGCGCA
 AAACTTAGGAAGGGTCAACGGGCAACCGGTGCCCTGCATCCCTGCTTCATGGCATCCGACGTGGTCAAGCTCGTTCAG
 CGCCGAGTAG

>ORF15675c (SEQ ID NO:232)

TCCTTCGGCCGGAACTGCATCAGCAGCCTCGGGCTCCTGAGCGGTGTCAAGCAATATCCCTGACAAACCCAAAGAACACGCG
 CATAGCGCTCGTCAACTAAAAAGACCCGTGTACAGAGATGGAGAGCTATGTCACCAATGGTGGTCCCTGCCTCGTCC
 AGCATGGCGACAAGCCTCGACCGCAGCGCTCGCAATACATCCGGCACGTCGGCCGGTCAAGAGCCGAGGCC
 CGCCAGGCGCGGGCTGAATTCCGGAGCAGGCTCATCGCCGCAACTCATTGCCGGCCTTCACAGCTGCAACGATCGGT
 G

>ORF16405 (SEQ ID NO:234)

ATCGACTTTGAGGAATGCGGGAAAGCCCTGGAAAAGTGTGTTCCCTGCAAGAAAGAAATAATTGATGTCATGCCAT
 TCGTTGTCGGCAGTGCAGGCTCCAAAGGCTGGGAAGGTTCATGAGCTCTCAACCTCAGTAGTTGCCTGGTCTTA
 GCCTTTATCAATCGCTGCCACAAAACCTGTGGAGCGATTGTCATGCCAGCGAGCAGAGCTACAAATCTCCATCACG
 GGTGGTGAATTACAAGCTGCCAGCTTATGTCACCAATAACGGGTCAAAGCCTGCAACTTTAGTTCCCTGAAATCAC
 ATCGAAAGCCACGACCAATCGAAAATGGTTTGGTAAGCAATACGGATGGCGAAATTCTGGAGGCCAGGCAAACCT
 AAAAAATAGGGCCTAACCGATGAGTCTATCCAAAAAATGTCGAAGCTGAGCGCTGGACGATTTGAAGTCTCAGTAC
 GCACTTGAGATAATTGCAATTACCGCTAAATACATAGAGGCCACGGGAGAAGGTTGTGCGTGTGCAACCGTTCAT
 GTGCCACACACCTCTGAAAGGGTGGCTGCCCTGGTAAACCTGGCATACCCATTGGTACCTGGTCAAGAATGAA

>ORF16925 (SEQ ID NO:236)

AGGCCACGGGGCAGAAGGTTGTGCGTGTCAACCGTTCATGTCGACACACCTCTGAAAAGGGTGGCTGCCCTGGT
 AAACCTGGCATACCCATTGGTACCTGGTCAAGAATGATGTTTATGCCCTGGGTTGACGCCGATTAAGCAA
 GCTGTGTTGCTCATCCAATACGTCCTCGCCAGTTAACGACTGTTATGTATATGGGTGCTGCCGCTACGTAATACCT
 TGGCCCTACGCTACCGAAGTTAATTGCAAGGCTCAATGGACAATCTCCTCTCGCGCTGACTGCAGCGGTAAAGGT
 GATCTACTTCGAAACACTGCAAGGGTAGGTCTTTGGCAGCGTCCATACCGACCGTGGTATGGCTCAGATGCC
 TGGTACTGCATTTACCAAATAA

>ORF17793c (SEQ ID NO:238)

GCCAAAATGATTGTCAATTGACAAAAATCTAGAACATCTTGTGCGCAATGCGCTATATGTGAAAAAAACTTTATTTGACGA
 GTTTTCTCTCAAGATTCAATTGGGGCATACTATTACGAGCCTAAATCTTGCCTCTGCAAGCATTGATATGGT
 CGCATCCAGCCCCGTGACGTTTTGGAACCAAAGAAATTCAAGAAAATTGGTGTGAAATCCGGTAGCAAGTC
 ATCACCTGAGTAAACATCGATAAAAATACCGTTAGATTATTTGGTCTGGTCAAACCAAAGGAACCTTGCGCGATT
 GTTGTGAGGTAACTGTAATGACGGTCAGGTAGAGCCGGGTTGACGGTAGTAACTGAAATCGTAAATATGT
 CGCCTGGAGATAGAAATACCGGCCGTAGCGATATAGCACAACTTATTTGGTAAATGCACTACAGCGCATCTGAG
 CCATACCACGGTCGGTATATGGACGCTGCCAAAAAGGACCTACCTGAGTGGTTCGAAAGTAG

>ORF18548c (SEQ ID NO:240)

AGGACAATGGCAGGGTGGCCGCGTCTCGCAGCCAAGGACGAAGGACAAATCTGATGAGTGTGTTACAGATCAAAGGGCG
 TACAACGAAATCCCACCGGATTGACGCGGCATCGTACTCCAGCAACAGCCTTAACTCACTGATGCAGGGGACGAGA
 GAATTGAAGAGTTTCCCTCGAATTGTCGTGGTGAAGGGTGGAGTGTAACTATTCTGCAACGACAAAACCTGTGG
 CGCATTGTCGATGGTATGACGATCAGGGTCACGATTCTGTTGGTGGAGGCCGTGAAGAAATCAAGGTGCCACAA
 TCGGTACGGCATAGTCTACCTACGGGAAGTCTTCTCAGCGCGGTGCTGGTGTCTCGCGAAGGTCGAACCTG
 CATTGATGGCAAGCTAAGCTCAGGATATTCAACACCCAACAAAATGTCTGCCCTACCAAAGGCGAGAAGCTTGGC
 TCTGTGATTTCACAGAACGACGCCACACCAAGCCCCATCAAGCGTGGCAGTGAATAATATCGACGCTTCCCAT
 CACCGGGCGCGCGATTGAAGAAGTGGTTTCGCTCAATCCCACCATATGGGTGGGCGCTGAATTAAATCGGAA
 GTTCCCTGGTGTCTCTTATAATGTACGCCGTATTACAAGGTTGTGCTGGAACACCAGTCGCAGCCTCAGTCA
 CAACAAAACGCTCAGCCATCGCCGAACGAAGTTAACGACAAATGA

>ORF17875 (SEQ ID NO:242)

ACGGCGTACATTATAAGAGAAGACACCCAGGAACTTCCGATTAAATTCAAGCGTCCACCCGACCCATATGGTGGGATTGAG
 CGAAAACCAACTTCTCAATCGCGCGCCCGTGTGGAAAGCGTCGATATTTCAGTCCACCGCTTGTGATGGGCTTTGGG
 TGTGCGTCGATTCTGTTGGAGAAAAAAATCACAGAGCCAAGCTTCTGCCCTGGTAAGGCAGACATTGGTGGTGGT
 TTGAATATCCTGAGCTTGAGCTGCCATCAAATGCAGGTTGACCTCGCCGAAGCAACAGCACGCCGTGAGAGAAA
 AAGACTTCCCGTAGGTAGGACTATGCCGTACCGATTGTGCGGCACCTGATTCTCAGCGGCCTCCACCAACAGAAT
 CGTGA

>ORF18479 (SEQ ID NO:244)

TCTGTAACACACTCATCAGATTGTCTTCGCTTGGCTGCGAGACGCCACCCCTGCCATTGCTTATACCGGC
 CGATATCCCCGGATACGCCCTGAAAGATGACGTGCGCAAAGCGTCGACCAATCTGAATTCAAACGCCCTGCTGTGATTG
 TTGGTGGCGCGAACGTCATGCCCTACATAACCTGGAGGGCAGCACACTGGAACGTTATCCCGCTTCTGAACAG
 CGTCTCTCGGAAAAAAAGCGCCCGCAGATCTCCGGCAGATCGAATTCTCATGGTGTGCCAGATAAGCTTGC
 CCGGTTCCATGACGAAGCAGTCATCCGGCTGCGAGCACCTCGCTGGCAGGGGTGCGTAGATTCTCGCAAG
 CTTCCACCCCTACTGTCAGGCGAGAGAGGCCCTGCGAGTGTAGGTCAAATCAAACGCCCTCCGGGTGGTCAACTCACG
 GTGGGCAAGGTGCTTGTGATTAG

>ORF19027c (SEQ ID NO:246)

ATGATTTACTCACCGCACTCGCTCTGAAACTGGTCCGGATGGAAAACAATCAAGCACCTGCCACCGTGAGTTGAC
 CACCCCGGAAGGCGTGGATTGACCTCAGACTCGCAGGCCCTCTCGCCTGACAGTAGGGGGTGGAAAGCTTGCAGAAT
 CTACCGCAACGCCCCCTGCCAGCGAGGTGCTCGCAGACCCGGATGACTGCTCGTATGGAACCGGCAAGACTTAT
 CTGGCGAGCACCATGAAAGAATTGATCTGCCGGAAAGATCTGGCGGCCCTTTTCCGAGAAGCACGCTGTTGAGAAG
 CGGGATAACGTTAGTCCAGTGTGCTGCCCTCAGGTTATGTAGGGCCGATGACGTTGCGCTCACCAACAATCACAGCG
 AGGGCTTGAATTCAAGATTGGTGCACGCTTGCACGTCATCTTCAGGCGGTATCCGGGATATCGGCCGTATAAAG
 GGACAATGGCAGGGTGGCCCGTCTCGCAGCCAAGGACGAAGGACAAATCTGA

>ORF19305 (SEQ ID NO:248)

TGGCCGTTCTCTGCCCTGCGCTTGGCATGACTGGTCAAGTCGGATGCAACCGGTGGTCAGCACCAATGCAATTGGG
 TGGTCATGTGCGATGCAATTACCGAGTTGAGGCTGGCCAGTTCTCCAAGCAAGCATAAGACCAAGATGGCACATTG
 CCAACAAAATACCCCTCCCGTACCGTTTATGCTGTTGCGCAGCCCTGATCTGGCGAAAAGCCCGTCCATGAA
 TCGTCATGGAGCCTCCATGTTCAACTCCTCTGGATATCCAGGAAGCCGCCCCACCCAAACAACCAAGCTGCC
 CCAGGGGATTCATCCTCCTCTGA

>ORF19519 (SEQ ID NO:250)

TCTGGCGGAAAGCCCGCTCCATGAATCGTATGGAGCCTCCATGTTCAACTCCTTCCTGGATATCCAGGAAGCCGT
 CCCCCACCCCAACAACCAAAAGCTGCCCCAGGGGATTCATCCTCCTGAGCAGCAGTGGAACTGCTCGGCACGCCCTCGC
 CGCCGGCAGCTACTGGAGAACATCTGGCAGCGCCTCGCTATCCAAGCAGCAATTGAGGAGATCTACCGGGGGCCACT
 GGCCAACATATGCCAGCTGGTCCAGCAGCTCCCTGCTCGAAAATCATCACCAGGCCATCCAGGCGGGATGATCGACAG
 ACAGCCTGGAGATCGTGGCTACGCACCAAGGTACGGCAGACCTACCTGCTCCGATCGGCGAGCAGCTGGCCAACTATGCC
 GAGCTGGCTACAGCAGCTGGTCCAGCAGCTGGCCACTGGCCAACTATGCCAGGCTGGAGATCGTGGCCACTACGC
 ACTCAAGGTACGGCAGACCTACCTGCTCCGATCGGCGAGCAGCTGGCCACTGGCCAACTATGCCAGGCTGGAGATCGTGG
 CCGCCGCGCGTATGGCCCTGGCTCATGACATAGGCAAGATCGTCGACCTGCAAGGTTGAGCTACAGGACGGCAGC
 ACCTGGCACCCCTGGAACGGAGCAACCCAGCCATACCCAGCTCAAGTACGTGAAGTCCCGGAATACCAGCTCCACGG
 CGCTGCCTCAGCACTTCATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTCCAGAGGCTGTGG
 CTCAATTGATCTACCTGTTGCTGGCAGTACGAGCAGCAGCCGGATCTCGCGAGATCATCGTGAAGGCAAGCAGG
 TCAGTTGCACAGGAGCTAGGAGCAATCCGGATCGAGCTCGCTGCACCGAAGCAGTCGCTGCAGCGGAGTTGGCAGA
 CGGCCCTCGCTTGGTAAGGACAAGTCAAGTGAATCAACCTAGCGCCGCTGTGATGGATGGCTGACCCAGGACG
 CACTCTGGCTGGTGAGCAAGCCTGCGATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGTGCCCCTCC
 TCTAACCGCCGTTCTCAGCATGCTCCAGGACCAAGCCGATCCAGACAAATGCCAGGACAAGGCCATTGGACGGC
 CACGGTAGACAACGGTGTGGATGGAAAACAAGTCAAGCTACTCAAGATTGCTCAGCCTTGATCTGGACAGATGCTG
 CCGAGCGCCCTCACCCCTACAGCGGATCACTGGCTGTGAAGATGGAACCGCCTCAACGGAAAGCCGGAAACGACCTG
 GAAATTCCAACGGGCCGGCTGAACAGCAGCAAGCAGCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGT
 GAAACCGGAAACGAGACGCAGGGATTGCAACCCCTCACTGATGATCAAGAAGAAACAGACGATTTGTATGCAC
 TTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGGCCACGACTGCCGGCTGCCCTCCTACGAACACACGCC
 GAGGAGAACCTACAGCAGGCCACTAGGGACCAAGGAGCAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTT
 TAGCAGAAGTACTGATCTGGACAGGGATTGTTGGATGAAATCTGGCATCGCGCCGCTGCCCTGTTCATCAACG
 ACACCAAGGTTGGTGCATACCGTAGACGGGACGCCATGCTGGTCAGCCAGGAATTTCAGGCTATGTCAGAG
 CATCCGGTGGTTGAAAAACTGGCCAAGGAGACGACCCGGCTGGAAGCTGGTGCAGCGCGCTCGAAGG
 GCTTCATCGGAAGACCAAGTAAAAACCTGAACATCTGGACCATCAAGGTTCTGGTCTCGAAGACGAAAGAGCTCAAG
 CCTACCTGCTCCAGGATCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAGCCTCACGGTAC
 GAAGGAGGTGTGGAATGA

>ORF20008 (SEQ ID NO:254)

GCTACAGGACGGCAGCACCTGGCACCCCTGGAAACGGACCGATCAACCAGCCATACCGCTCAAGTACGTGAAGTCCCG
 AATACCAAGCTCCACGGCGCTGCCCTAGCACTTCATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTC
 TTTCCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGCAGTACGAGCAGCAGCCGGATCTCGCGAGATCATCG
 GAAGGCAGACCCAGGCTCAGTGACAGGAGCTAGGAGGAATCCGGATCGAGCTCGCTGCACCGAAGCAGTC
 AGCGGCAGTTGGCAGACGGCTTCGCTTGGTGAAGGACAAGTCAAGTGAATCAACCTAG

>ORF20623c (SEQ ID NO:256)

CGTGAACCTGTTCTCCATCCAGCAGCGTGTCTACCGTGGCCGTCAAATGGCCTGTCCTCGGCATTGCTGGATGA
 CGGCTTGGTCTGGAGCATGCTGAAGAACGGCGTTAGAGGAGGGCACCCCATCGATAACCTGGCCAGCAGGTAGGCT
 CTCAGTTGATCGGCAGCAGGCTTGCTCAGCAGCCAGTGTGCTGGTCAAGCAGCAGGGCCGCTAGGTTG
 ATTCAACTTGAACCTGTCCTCAGCAAGAAGCGAAGGCCGCTGCCAACAGCAGCAGCTGCTTCGAGCC
 GAGCTCGATCCGGATTGCCCTCTAG

>ORF21210c (SEQ ID NO:258)

CGCTTGAAAATTCTGGCGTGCACAGCATGGCGTCCCGTCTACGGTATGCACCAAAGCCTTGGTGTGTTGATGAACAG
 GCGACGGGCCGCGATGCCAGATTCTACCAACCAACGAATCCCTGTCCAGATCAGTACTTCTGCTAGGCATAAAATACAT
 CTTCAATTGCTTCAGGAGCGCAATCTGTTGGCTCTGGTCCCTAGTGGCTGCTGTAGGTTCTCCTCCCCGGTGTGTT
 GTAGGAGAGGCAGCGCGAGTGTGGCTAGTGTCTAGCTTCTAGTGGGAATTGATATTACCAAGAAGTCATACAA
 ATCGTCTGTTCTTCTTGA

>ORF21493c (SEQ ID NO:260)

GCTGCTGGCGTCATTCCACACCTCCCTCGCATCGGTATGACCGTGAGGCTTGGTTGTCCAGAGGCTGCTCAGGGA
 ACAGCAATTGGGATCTGGAGCAGGTAGGCCTGAGCTCTTCGCTTGCAGGACAGAAACCTTGTGATGGTCCAGATG
 TTCAGGTTTTACTGGTCTCCGATGAAGCCCTGTTTCGAACGCGCCTGCACCCAGCTTCAGGCCGTCGTCTCCT
 GGCTTGGCCAGTTTCAAGCACCGGATGCTCTGGACATAGCGCTGAAAATTCTGGCGTACCCAGCATGGCGTCC
 CGTCTACGGTATGCACCAAAGCCTTGGTGTGTTGATGACACAGGCGACGGCCGATGCCAGATTCTACCAACCAAC
 AATCCCTGTCAGATCAGTACTCTGCTAGGCATAAAATACATCTCAATTGCTTCAGGAGCGCAATCTGTTGGCTCCT
 GGTCCCTAG

>ORF21333 (SEQ ID NO:262)

ACATCTGGACCATCAAGTTCTGGCTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCAAATTGCTG
 TTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTATCACCGATGCCAAGGAGGTGTGGAATGACGCCGAGCAG
 CTCACCGAGGAGTACATCTCGCGCACGATCTCCGGGAAGCCAGCGCAAGATCTACCGCGCCGACCAAGGCGTCTG
 CAAGCACCTCGGTCTACGGCAACCGTACAGGACGTGGACCACCGGGTGTCTGGGATGGCGACGCAAGGTACTGGAAC
 AAGGCCTGTCAGCGGAGCTGGAAACACGTACTCGAATCATCGCGGACGATCTGGGGTATGCCATCGAGCATGA

>ORF22074c (SEQ ID NO:264)

GTGAGGCACAAGCCCTCCGTTATTGGCACTACGAACCTTTGTGAGTCTTCTCTGCTCGCCGCGGATGAGGATCAGT
 GATTTTCCCAGTCGATGTCGCGCTTGGGATGCACAACAGCGCATTCAACCGGATGCCGGTGAAGTAGAAGACCTCAAAC
 GTGCAAAGCCAGAACCAAGGCGGGGTGATCCGTGCGTTGCGCCGGTGCAGCGCTGCGCCGTCCTGCATTTGAGCCA
 ATTGCGGGCGAGCAGGATGGCTTCGGCGCGACGGTTTGCTTGCTCGCCTGGGGGAATGACGGTGGTCTTCTGAACG
 GGTTGACTTGGGAGTGCACCAACTCATGCTGATGGCATAGCCCCAGATCGTCCGCAGATGATTGAGTACGTGTT
 CAGCTCCGCTTGGACAGGCTTGTCCAGTACCTTGCGTCGCCATCCAGGACAGCCCGGTGGTCCACGTCTGTACGGT
 TGCGTAGGACCGAAGTGTGTTGAGCAGCGCTTGGCGCGGTAGATCTCGCCTGGCTCCCGGAGATCGTGC
 CGAAGATGACTCCTCGGTGAGCTGCTCGGGCGTCACTCACACCTCTCGGATCGGTGATGACCGTGAGGCTTGGG
 TGTCCAGAGGCTGCTAGGGAAACAGCAATTGGGATCTGGAGCAGGTAG

>ORF21421 (SEQ ID NO:266)

CGAGCCTCTGGACAACCCAAGCCTCACGGTATCACCGATGCCAAGGAGGTGTGGAATGACGCCGAGCAGCTCACCGA
 GGAGTACATCTCGCGCACGATCTCCGGGAAGCCAGCGCAAGATCTACCGCGCCGACCAAGGCGTCTGCTCAAGCACT
 TCGGTCCTACGGCAACCGTACAGGACGTGGACCACCGGGTGTCTGGGATGGCGACGCAAGGTACTGGAACAAGGCTG
 TCCAAGCGGAGCTGAAACACGTACTCGAATCATCTCGGACGATCTGGGCTATGCCATCGAGCATGAGTTGGTACGCA
 CTCCCAAGTCACCCGTTCAAGAAAGACCAACCGTCACTCCCCCCCAGGCGAGCAAGCAAACCGTCGCCGCCGAAAGCCATCC
 TGCTCGCCCGCAATTGGCTCAACATGCAGGACGGCGCAGAGCGCTGCACCGCGAACGCGCACGGATCACGCCGCGCTGG
 TTCTGGCTTGTGACGTTGAGGTTCTACTTCACCGGATCCGGTGAATGCGCTGTTGTCATCGCAAGCGCAGCAT
 CGACTGGAAAATCAACTGATCTCATCGCGGGGAGACAGAGAAAGACTCACAAAGAGTTGAGTGCCTGCAAAACGGAGG
 GGCTTGTGCTCACCTATCGAGGCTCTGCAAGAGGCCATAGAGCCGATTGCGCGATGACGACCGAGTTGTCACGTC
 AACCGGTTCTCACCGCACTACAAGAGCAAGGTGATGAACTCCGACCGTGAAGGCGATGACCGGAGTTGACCGAGAA
 GGTTGGGGTGCAGGATGACCCCGCACCGTTCCGGCACACCCCTGGCACCGACTTGATGAGGCAACCGAGCGGAAACATT
 ACCTCACCGAAGTGCCTGCTCACCAACTCGAATATCCAGACCGATGAGCTACATCGAGGCCACTACGATCACATGCGT
 GCCGTGCTGATGCTAGAAGCCTGGCCAAGGCCGCTGGAGAATGTCAGGAAGGTGGATTACAGCGGCTCCCGCAAGC
 CTCTGCCAAACCGAAGCCATGCGGGCAACCTCTCGCTCGAGTGTAGTGAAGCGCCGCCACCGGAGGCCAGGACAGAGCCTG
 CAGAACCAAGGGAGCACGCCAGGGACAGGCAATTAGGGAGGTCCAACCGCGTGGGAAGCAGATGCGCTACCAACAGCCA
 CCTGACACCTTCGAACCAAGCGTGTGTTACTCTGATGCGCTAAACATTATCGAACCGTGCCGCCCTGGCATCCGCGC
 TCCCGCTGCAACAAGCGGATCAGGCCGATGGGATCTGCCGCCGAAGCAATCTGCCCTAG

>ORF22074c (SEQ ID NO:264)

GTGAGGCACAAGCCCCCTCCGTTATGGCACTACGAACCTTTGTGAGTCTTCTCTGTCTCGCCGCGATGAGGATCAGTT
 GATTTCCCAGTCGATGTCGCGTTGCGGATGCAACAGCGCATTCAACCGGATGCCGGTGAAGTAGAAGACCTCAAAC
 GTGCAAAGCCAGAACCGAGCGGGCGTGTACCGTGCAGCGCTCTGCCGCGTGCAGCGCTCTGCCGCGTGCATGTTGAGCCA
 ATTGCGGGCGAGCAGGATGGCTTGGCGCGACGGTTGCTTGTGCTGCCCTGGGGGAATGACGGTGGTCTTCTGAACG
 GTTGACTTGGAGTGGCTCACCAACTCATGCTGATGGCATAGCCCCAGATCGTCCGCAGATGATTGAGTACGTGTC
 CAGCTCGCTTGGACAGGCTTGTCCAGTACCTTGCCTGCCATCCAGGACAGCCGGTGGTCCACGTCTGTACGGT
 TGCCGTAGGACCGAAGTGGCTTGAGCAGCGCTTGGTGGCGCGGTAGATCTTGCCTGGCTCCGGAGATCGTGC
 CGAAGATGTAACCTCTCGGTGAGCTGCTGCCGCTCATTCCACACCTCTCGGCATCGGTGATGACCGTGAGGCTGGT
 TGTCCAGAGGCTGCTAGGGAACAGCAATTGGATCGGAGCAGGTAG

>ORF21421 (SEQ ID NO:266)

GCAGCCTCTGGACAACCCAAGCCTCACGGTATCACCGATGCCGAAGGAGGTGTGGAATGACGCCGAGCAGCTACCGA
 GGAGTACATCTCGCAGCATCCGGAAAGCCAGCGCAAGATCTACCGCAGGCCACCGGCTGTCTGGATGGCAGCAGGACT
 TCGGTCTACGGCAACCGTACAGGACGTGGACCAACGGGCTGTCTGGATGGCAGCAGGACTGGAAACAAGGCTG
 TCCAAGCGGAGCTGGAACACGTACTCGAATCATCGGGACGATCTGGGCTATGCCATCGAGCATGAGTTGGTACGCA
 CTCCCAAGTCACCCGTTAGAAAGACCAACCGTCAATTCCCCCAGCGAGCAAGCAAACCGTCGCGCCGAAGCCATCC
 TGCTCGCCCGCAATTGGCTAACATGCAAGGACGGCGCAGAGCGCTGCACCGCGAACCGCACGGATCACGCCGCTGG
 TTCTGGTTTGCACGTTGAGGTCTTCACTTCACCGGACATCCGGTGAATGCGCTGTTGTGCATCCGAAAGCGACAT
 CGACTGGGAAATCAACTGATCCTCATCCGGCGAGACAGAGAAAGACTCACAAAGAGTTCGTAGTGCCTAAACGGAGG
 GGCTTGTGCTCACCTATGAGGCTCTGCAAGAGGCCATAGAGCCGATTCGCCATGACGACCAGTTGTTCAACGTC
 AACCGGTTCTCACCGACTACAAGAGCAAGGTGATGAACTCCGACCGGTCGAAGCCATGTACCGGAAGTTGACCGAGAA
 GGTTGGGTGCGGATGACCCGACCGTTCCGGCACACCTGGCACCGACTTGTGAGGACCCGAGCGGAACATT
 ACCTCACGAAGTGCCTGCTCAACCAACTCGAATATCCAGACCGATGAGCTACATCGAGGCCACTACGATCACATGGT
 GCCGTGCTGATGCTAGAAGCCTGGCCAAGCGCGCTGGAGAATGTCAGGAAGGTGGATTACAGCGGCTCCCGCAAGC
 CTCTGCCAAACCGAAGCCATGCGGCAACCTCTGCTCGAGTGAAGCGCCACCGGAGGCCAGGACAGAGCTG
 CAGAACCAAGGGAGCACACGCCAGGGACAGGCATTAGGGAGGTCCAACCGCTGGAGCAGATGCGTACACAGCCA
 CCTGACACCTCGAACCAAGCGTGTGTTACTCTGATGGCTAAACATTATGAAACCGTGCCTCGGCATCCGCGGC
 TCCCGCTGCAACAAGCGGATCGGAGTGGGATCTGCCGCCGAAGCAATCTCGCCTAG

>ORF22608c (SEQ ID NO:268)

CGCATCTGCTTCCCACGCCGGTGGACCTCCCTGAATGCCGTGCTCCCTGGCGTGTGCTCCCTGGTTCTGCAGGCTCTGTCC
 TGGCCTCCGGTGGCGGGCTTCACTCACTCGAGCGAGAGGTTGCCGCTGGCTTGGCAGAGGCTTGCGGGAG
 CCGCTGTAATCCACCTCTGACATTCTCCAGCGCGCTGGGCCAGGCTCTAGCATGCAAGCACGGCACGATGTGATC
 GTAGTCGGCCTCGATGAGCTACGTTGAGTGGATATTGAGTGGTGAAGCAGGCACCTCGTGAGGTGAATGTTCCGCT
 CGGGTGCCTTCATCAAGTCGGTGGCCAGGGTGTGCCGAAACGGTGCAGGGTCACTCCGCACCCCAACCTCTCGGTCAAC
 TTCCGGTACATGGCTCGACCTGGTGGAGTTACACCTTGCTTGTAGTGCAGGTGA

>ORF22626 (SEQ ID NO:270)

CACCTTCGAACCAAGCGTGTGTTCACTCTGATGGCTAAACATTATGAAACCGTGCCTCGGCATCCGCGCTCCG
 CTGCAACAAGCGGATCAGCGGATGGGATCTGCCGCCGAAGCAATCTGCCAGCGATACCGTACTGAGGGCCGGCT
 ACCGGACGAAAGGTAGCGTGCCTCCAGCAGATCGTTAGGCCTGTAGGAAAAATCTGGAATTACCGAGAGCGCCTGGAT
 TCCAGCGCCGGCATGTCGGCAGAGCCAGCGCAATTCAAGGCCAATACCACAGTACCCCTCTGTAATCGCTGA

Fig. 3-19

>ORF23228 (SEQ ID NO:272)

AGAGATTGAACTCCCACATCCTGCTCCAAAGCAGGCGCCTACCGACTGCGCTATAACCCGATTGGAATTGGCTC
 CGGCACCTGGACTCGAACCGGACCAATGATTAACAGTCATTGCTCTACCGACTGAGCTATCGCGAACGTCTTCT
 TCCAACCTGGACGCTTCCGGTGTGCTGGATCGCGTCTCAGAGGCGGCCATTACGGATGCGCGGGCATGTCAA
 CCCTCTGATCCAAAAGTTTCTCTTTTCCACGAGGACAAAACGGCCCTTCACTGCATGCGGAGCGCTCTCGCG
 CCTACCGGACGCCATGAAAAAGCCCCGCCAAGCGGGGTTCCCTGTCGCCCGGAAGAGGTCAAGGCCAGACGATC
 TCGTCGCTTCCACCTCGCGAGATACTGGCACCCGGCGCAATTGCGGCCAGGATCAGTGCAGGCCAGCGGGTTCTC
 GATCCAGCGCTGGATGCCCGCTTCAGCGGGGTGCGCCATAGACCGGGTCGAAGGCCAGGCAATCAGCTTGTCCAGCG
 CCTCCTGGCTCAGTTCAGGCTCAGCTCGCGCTCGGCCAGGCCTGCGCAGGCAGGAGCTGGATCTGGCGATGCCG
 GCGATCTGCTCGGAGGCCAGCGGCTCGAACACCACCTCGTCGATCCGGTTGATGAATTCCGACGGAAGTGGCATT
 GACCGCGTCCATCACTGCGGCACGTTGCGCCTCGCGGTGCCAGCTCCTGGATCTGCGGCCAACCGAGGTTGGAGG
 TCATCACCAACACGGTGTGCGGAAGTCCACCGTACGCCGTACTGCGGTCAAGCGTCCCTGAGCACCTGGAGG
 AGAATGTTGAATACATCCGATGGCCTCTCCACCTCGCCAGCAGCACCCAGTAGGGCTGCGGCCATGCC
 GGTCAAGTAGCCGCTTCTCGAACGCGACGTAGCCGGAGGCGCGCAGTACGGCGGCCACCGAGTGTCTCCATGA
 ACTCGGACATATCTATCCGACCGCCTCTCGTATCGAAGAGGAACCTGGCCAGCGCCTTGCACAAACTGGCTTG
 CCCACCCGGTGGCGAGGAAGAGGAACGAGCGCTCGGCCGGTTCGGATCGCGAGGCCGCGCACCGCG
 GCGTGGACACGGGACTACCGCCTCGTCTGGCGATCACTCGCCGATGCAAGCTCTGCTCATGCCAGCAGCTTCT
 CGCGTCGCCCTCGAGCATCTCGACACCGGATACCGTCCACTGGAAACCAACTTCCGCGATTTCCTGCGGT
 TTGTTGCGCAGCAACTGGTCTCGTCTGGTGTGCGTGGTCACTGCAAGGCTGCGTCCAGGTCCGGGATGGTCTG
 GTACTGGATGCGCGCATGCTCTCGAGGTGCCCTGCGCGGCCGCTCCATCTCTGCTGGCCTGCTGATCTTCT
 GCTGGATCTGCGCGAGCCCTGACCTCGGCCCTCTCGGACTTCCAGATCTCTCGAGGTGGCTATTGCGCTCGAGC
 TTGACGATATCTCTCCAGCTGGCCAGGGCCTCTGGTGGCTCGTCTCTCTTCTCAGCGCCTCGCGCTCGAT
 CTTCAGCTGGATCAGCGACGGTCAAGACGATCCAGTCTCCGGTGGAGTCTCCATGCGGATGCGGCTGGCG
 CCTCGTCGATCAGGTGATGGCCTGTCGGGAGTGGCGATCGGTGATGTAAGCGGTGCGACAGCTGGCGCG
 ATCGCGCCGTCGGTGTGTCACCCCGTGGTCACTTCATAGCGTCTTGAGGCCACGGAGGATGGCGATGGTGTCTC
 CTCGCTGGTCTCGTCCACCAGCACCTCTGGAAGCGGCCCTCAGCGCGGACATCTCTCGATGTAAGCGGATACTCG
 CGAGGGTAGTAGCACCGACGCGAGTCAGCTCGCCGCGGCCAGAGCGGGCTTGAGCATGTTGCCGGTCCATGGCACCT
 TCCGCTTGGCGCCGACCATGGTGTGCACTGTCGATGAACAGGATGACCCGGCTCTCGTGTGCCAGTTGCGT
 GAGGACCGCCTTCAGGCGTCTCGAACCTGGCGGAACCTGGCACCGCGATAGCGCCCCCATGTCAGGCCAGCA
 GGCGCTTGTCTTGAGGCCGTCGGCACCTCGCCGTTGATGATGCGTGGGCCAGGCCCTCGACGATGGCGGTCTGCG
 ACGCCGGGTTGCCGATCAGCACCGGTTGTTCTGGTCGCCGCTGCAAGGACCTGGATGGTCCGGCGGATCTCGTC
 GCGACCGATCACCGGTCGAGCTTGCCTTCTCGGCCGCTGGTCACTGCAAGGTGACTCTGTCAGCGCCTGGCG
 ACTCCCTGACGTTGGTCTCACCGCTTCCGCGCCACGCAAGGTGGCCAGGCAATTCTCAGCGCCTGCGGACACG
 CCCTGGCCGAGCAGCAGCTTGGAGGCCGCTGGTCTCGTCCATCGCGGCCAGCAATACAGCTCGTGGAGATGAACG
 GTCGCCCTCTGCTGGCCAGGGCGTCAAGCTGGTGTGAGCAGGGCGTGGAGATCTGGACAGGTTACGTCGCG
 GGCTCTGGATCTCGGCAGCGCGTCACTGGTGTGAGGCGCTGCGCAGGGCGGATATCGAAGGCCACCTGCA
 AGCAGGGGCTGATGAAACGCCCTGCTGCTCGAGCAGGGCGGAAAGCAGGTGCAACGGCTGATGGCGGATGGTCA
 GCCAACGGCCAGGGACTGGCGTCGGAGAGGCCAGTTGCACTGCTGGTCAAACGGTCTATTGCGATGGTCTT
 CCTCTATAG

>ORF23367 (SEQ ID NO:274)

GCTATCGCGAACGTCTTCTCAACCTGACGCTCCGGTGTGCTGGATTGGCTCTCAGAGGCCGCCATTAC
 GGATGCGCGCGGGCATGTCACCCCTGATCAGGAAAGTTTCTCTTCCACGAGCGAACAAACGGCCCTCCACT
 GCATGCGGCAGCGCTCTCGCCCTACCGACGCCATGAAAAAGCCCCGCCAAGCGGGGTTCCCTGTCGCCCG
 AGAGGTCAAGCGAAGACGATCTCGTCGCCCTTCCACCTCGCCGAGATACTGGCACCCGGCGCAATTGCGGCC
 CAGGATCAGTTGCGCCAGCGGGTCTCGATCCAGCGCTGGATGGCCGCTTCAGCGGGCGCCATAG

>ORF25103c (SEQ ID NO:276)

AGTGCACCAACGGGGT GAGCAT CACCGACGGCGCATCGCCGGCCAAGCTGTCGACCGCTACATCACCGATCGC
 AACTGCCGACAAGGCATCGACCTGATCGACGAGGCCAGCCATCGCAGCTGAGATCGACTCCAAGCCGGAGGAA
 CTGGATCGTCTCGACCGTCGCCCTGATCCAGCTGAAGATCGAGCGCAGGGCGTGAAGAAGGAAGACGACGAAGCCACCAG
 GAAGCGCCTGGCCAAGCTGGAGGAGGATATCGTCAGCTCGAGCGCAATACGCCGACCTCGAGGAGATCTGGAAGTCCG
 AGAAGGCCAGGTGCAAGGGCTCGGCGCAGATCCAGCAGAAGATCGAGCAGGCCAACGAGGAGATGGAGGCCGCGC
 AAGGGCAGCTCGAGAGCATGGCGCATCCAGTACCGACCATCCGGACCTGGAACGCAGCCTGCAGATGGTCGACCA
 GCACGGCAAGACCGAGAACCAAGCTGCTGCGCAACAAGGTGACCGACGAGGAATCGCGAAGTGGTTCCAAGTGGACCG
 GTATCCCGGTGTCGAAGATGCTCGAGGGCGAGCGCAGAGCTGCTGCGCATGGAGCAGGAGCTGCAATGGCAGTGC
 GGCCAGGACGAGGCGGTAGTCGCGTGTCAAACGCCGTGCCGTTGCCGCCGCCCTGCCGATCGAACCGCCAG
 CGGCTCGTCTCTCTCGGCCGCCACCGGGGGGGCAAGACCGAGGTTGTGCAAGGGCCTGGCCAGTTCTCTTCGATA
 CCGAGGAGGCGCTGGTGC GGATAGATATGTCGAGTTATGGAGAAACACTCGGTGGCCGCTGATCGGCGCCTCCG
 GGCTACGTCGGCTTCGAGGAAGGGCGTACCTGACCGAGGCATCCGCCGAAGCCCTACTCGGTGGTGTGCTGGACGA
 GGTGGAGAAGGCCATCGGATGTATTCAACATTCTCCAGGTGTCGAGGACGGACGCCGACAGTCACGGC
 GTACGGTGACTTCCGCAACACCGTGGTGGTGTGACCTCAACCTCGGTTGCCGCAGATCCAGGAGCTGGCCGGCGAC
 CGCGAGGCGCAACGTGCCGAGTGTGATGGACGCCGCAATGCCACTTCCGCGGAAATTCAACGGATCGACGAAGT
 GGTGGTGTGAGGCCGCTGGCTCGCGAGCAGATGCCGGCATGCCGAGATCCAGCTGGTCCGCTGCCAAGGCCCTGG
 CCGAGGCCGAGCTGAGCCCTGGAACTGAGCCAGGAGGCGCTGGACAAGCTGATTGCCGTCGGCTTCGACCCGGTCTATGGC
 GCACGCCGCTGAAGCGGGCCATCCAGCGCTGGATCGAGAACCCGCTGGCGCAACTGATCTGGCCGGAAATTGCC
 GGGTGCCAGTATCTGGCGAAGGTGGAAGGCACGAGATCGTCTCGCCTGACCTCTCGGGCGGACAGGGAAAGGCC
 CGCTTCGGGGGGCTTTTATGGCGTCCGGTAGGCGCAGAGCGCTGCCGATGCACTGGAAGGGCCGTTTGTGCGCT
 CGTGGAAAAAGAAGAAAAACTTTGGATCAGAGGTTGACATGCCGCGCATCCGTAATGGCGCCTCTGA

>ORF23556 (SEQ ID NO:278)

AAAAGCCCCGCCGAAGCGGGGCTTCCCTGTCGCCCGGAAGAGGTCAGGCCAAGACGATCTCGTCGCCCTCACCTTC
 GCCGAGATACTGGCACCCGGCGCAATTGCGGCCAGGATCAGTGGCCAGCGGGTTCTCGATCCAGCGCTGGATGGC
 CCGCTTCAGCGGGCGTGCGCCATAGACCGGGTCGAAGCCGACGCCATCAGCTTGTCCAGGCCCTCGGCTCAGTCCA
 GGCTCAGCTCGCGCTCGGCCAGGCCTGGCGACCGAGCTGGATCTGGCGATGCCGGATCTGCTCGCGAGCC
 AGCGGCTCGAACACCACCTCGCATCCGGTTGA

Fig. 3-21

>ORF26191c (SEQ ID NO:280)

AAGGAAGGACGACCCATGCGAATAGACCGTTGACCAGCAAGCTGCAACTGGCGCTCTCGACGCCAGTCCCTGGCCGT
 TGGCCATGACCATCCGGCCATCGAGCCGTGACCTGTTCCGCCCTGCTGAGCAGCAAGGCCAGTGCATCAAGCCCC
 TGCTGATGCAGGTGGCTTCGATATCGCCGCCCTGCGAGCGGCCCTCAACAAAGAACTCGACGCCCTGCCAGAAGATCCAG
 AGCCCGACCGGCACGTGAACCTGCTCCAGGATCTGCACGCCCTGCTCAACCAGGCTGACGCCCTGCCAGAAGGG
 CGACCAAGTCACTCTCAGCGACCTGGTATTGCTGGCCGATGGACGAGAACACCAAGGCTGCCAGCTGCTGCC
 AGGGCGTGTGCGCAAGGCCTGGAGAACATGCCAGCTGGCAACCTGCTGCCAGCGGCCAGGAAGGCAAGCTGACCCGAACGTCAG
 GAGTCGCCAGGCGCTGGACAAGTACACCGTCGACATGACCAAGCGGCCAGGAAGGCAAGCTGACCCGGTGTGATCGG
 TCGCGACGACGAGATCCGCCGGACCATCCAGTCCTGCGACGCCAGGAAGAACAACCCGGTGTGATGCCGAACCCG
 GCGTCGGCAAGACGCCATCGTCAGGGCTGGCCAGGCCATCATCAACGGCAAGTGGCGACGCCCTCAAGGACAAG
 CGCCTGCTGGCCCTGGACATGGGGCGCTGATCGCCGGTGCAGTCCCGCAGGCCAGTTCGAGGAACGCCCTGAAGGCGGT
 CCTCAACGAACACTGGCAAGCAGGAAGGCCGGTATCCTGTTCATCGACGAACTGCACACCAGGCTGCCAGGCAAGG
 CGGAAGGTGCCATGGACGCCAACATGCTCAAGCCGCTGCCGCCAGGCTGACTGCGTGGTGCTACTAC
 CTCGACGAGTATGCCAGTACATCGAGAACGGATGCCGCTGGAGGCCGCTTCCAGAACGGTGTGGTGACGAAACCGAG
 CGAGGAAGACACCATGCCATCCGTGGCCCTCAAGGAACGCTATGAAGTGCACACGGGGTGGCATCACCAGCG
 CGATCATGCCCGGCCAACGCTGCGCACCGCTACATCACCGATGCCAACTGCCGACAAGGCCATGACACTGATCGAC
 GAGGCCGCAAGCCGATCCGATGGAGATCGACTCCAAGCCGAGGAACGGATCGTCTGACCCGCTGCCGATCCAGCT
 GAAGATCGAGCGCGAGGCCGCTGAAGAACGGAGACGAGAACGCCACAGGAAGGCCCTGGCAAGCTGGAGGAGGATATCG
 TCAAGCTCGAGCGCAATACGCCACCTGAGGAGATCTGAAGTCCGAGAAGGCCAGGGCTGCCAGGAGGCTGCCAGATC
 CAGCAGAACATCGAGCAGGCCAACGAGGAGATGGAGGCCGCCAGGCCACCTCGAGAGCATGCCGCATCCA
 GTACCCAGACCATCCGGACCTGAAACGCAAGCCGCTGACGGACAGGGCACGCCAACGGAGAACCGAGAACGAG
 ACAAGGTGACCGACGAGGAATGCCGAAGTGGTTCCAAGTGGACCCGTTCCGGTGTGAGATGCTCGAGGGCGAG
 CGCGAGAACGCTGCTGCCATGGAGCAGGAGCTGCATGCCGAGTGATGCCAGGGACGAGGCCAGGGCTGAGTGCCTGTC
 CGCCGTGCCCGTTCGCCGCCGCTGCCGATCCGAACCGGCCAGGGCTGCCAGGGCTGCCGCTGCCGCTGCCG
 TGGCAAGACCGAGTTGTGCAAGGCCGCTGCCGAGTCCCTCTCGATACCGAGGGCGCTGGTGCGGATAGATATGTCC
 GAGTTCATGGAGAACACTCGGTGGCCGCTGATGCCGCGCTCCGGCTACGTCGGCTTCGAGGAAGGCCGCTACCT
 GACCGAGGCCATGCCGAAGCCCTACTCGGTGGCTGCTGGACGAGGTGGAGAACGCCATCCGGATGTATTCAACA
 TTCTCTCCAGGTGCTCGAGGAAGGCCGCTGCCGACAGTCACGGCGTACGGTGGACTTCCGAAACACCGTGGTG
 ATGACCTCCAACCTCGGTTGCCGCAAGATCCAGGAGCTGCCGGCAGGCCACGGCGCACTGCGCGCAGTGTGACGC
 GGTCAATGCCACTCCGTCGGAATTCATCAACCGGATCGACGAAGTGGTGGTTCGAGGCCGCTGGCTGCCAG
 TCGCCGGCATGCCGAGATCCAGCTCGGTGCCCTGCCAGGCCAGGCCAGCTGCCAGGCCAG
 GAGGCCGCTGGACAAGCTGATTGCCGCTGCCAGCCGGTCTATGCCGACGCCGCTGAAGGCCGACGCCG
 GATCGAGAACCCGCTGCCGCAACTGATCCTGCCGGCAAATTGCCGCGGGTGCAGTATCTGCCGAGGCC
 ACGAGATCGTCTCGCCCTGA

>ORF23751 (SEQ ID NO:282)

ACCGGGTCGAAGCCGACGGCAATCAGCTTGTCCAGCGCCTCTGGCTCAGTTCCAGGCTCAGCTCGCGCTGCCAGGG
 CTTGCCGAGGCCACGGAGCTGGATCTGCCGATGCCGGGATCTGCTGCCGAGGCCAGGCCAGGGCTCGAACACCAC
 CGATCCGGTTGATGAATTCCGGACGGAAGTGGCATTGACCCGGTCCATCTGCCGAGGCCAGGGCTGCCG
 GCCAGCTCCGGATCTGCCGAAACCGAGGTGGAGGTACCAACGCCACGGTGTGCCAGTCCACCGTACGCCGTG
 A

>ORF24222 (SEQ ID NO:284)

CCCGGAGGCCGCCGATCAGGCCGCCACCGAGTGTTCATGAACTCGGACATATCTATCCGACCCAGGCCCTCTC
 GGTATCGAAGAGGAACCTGCCAGGCCCTGCCACAACCTCGGTCTGCCACCCGGTGGGCCAGGAAGAGGAACGCC
 CGCTCGCCGGGTTGCCGATGCCGAGGCCGGGCCGCCAGGGCGCACGGCGTGGACACGGCGACTACCGCCTGCC
 CGATCACTGCCGATGCCAGCTCTGCCATGCCAGCAGCTCTGCCCTGCCGAGCATCTCGACACCGGGAT
 ACGGTCCACTGGAAACCACTCGCGATTCTCTCGGTGACCTGTTGCCAGCACTGGTCTCGGTCTGCC
 GCTGGTCGACCATCTGCCGCTCCATCTCTGCCGTTGCCGCTGCCGATCTCTGCCGAGGCCCTGCCAC
 TTGCCGCGGCCCTCCATCTCTGCCGTTGCCGCTGCCGATCTCTGCCGAGGCCCTGCCAC
 CTCGGACTTCCAGATCTCTGCCGAGGTGGCTGCCGATCTGCCGCTGCCGATCTCTGCCGAGGCCCTGCC
 TCCGGTGGCTCGCGCTCTCCCTCTGCCGCTGCCGCTGCCGATCTCTGCCGAGGCCCTGCCAC
 AGTTCTCCGGCTGGAGTCGATCTCATGCCGATGCCGCTGCCGCTGCCGATGCCGAGGCCCTGCC
 TTGCCGATCGGTGATGAG

Fig. 3-22

>ORF24368 (SEQ ID NO:286)

ACTCGGACATATCTATCCGACCAAGCGCCTCTCGGTATCGAAGAGGAACCTGGCCAGCGCCTTGACAACTCGGTCTTG
 CCCACCCCGGTGGGCGAGGAAGAGGAACCGAGCCCTCGGCCGTTGGATCGGAGGGCGCGAACGGCGCAC
 GGCGTTGGACACGGCAGTACCGCTCTGGCGATCACTCGCCGATGCAGCTCTGCTCCATGCGCAGCAGCTTCT
 CGCGCTCGCCCTCGAGCATCTTCGACACCAGGATACCGGTTGGAAACCACTCGGCATTTCTCGTGGTAC
 TTGTTGCGCAGCAACTGGTCTCGGTCTGCCGCTGGTCGACCATCTGCAGGCTGCGTCCAGGTGGATGGTCTG
 GTACTGGATGCGGCCATGCTCTCGAGGTGCCCTGCGCCGCGCCCTCATCTCTGCTTGGCTGCTGATCTCT
 GCTGGATCTGCGCCAGCCCTGACACTCGGCCCTCGGACTTCCAGATCTCTCGAGGTGGTATTGCGCTGAGC
 TTGA

>ORF24888c (SEQ ID NO:288)

AGAAGGAAGACGACGAAGCCACCAGGAAGCGCCTGGCAAGCTGGAGGAGGATATCGTCAAGCTCGAGCGCAATACGCC
 GACCTCGAGGAGATCTGAAGTCCGAGAAGGCGAGGTGCAGGGCTGGCGCAGATCCAGCAGAAGATCGAGCAGGCCA
 GCAGGAGATGGAGGCGGCCGCGCAAGGGCACCTCGAGAGCATGGCGCATCCAGTACCAAGACCATCCGGACCTGG
 AACGCAAGCCTGCAAGATGGTCGACCGACGGCAAGACCGAGAACAGTTGCTGCGCAACAAGGTGA

>ORF25398c (SEQ ID NO:290)

AGGCGGTCTCAACGAACTGGGCAAGCAGGAAGGCCGGGTCACTCTGTCATCGACGAACTGCAACACCATGGTCGGCGC
 GGCAAGGCGGAAGGTGCCATGGACGCCGGCAACATGCTCAAGCCGGCTGGCGCGGGAGCTGCACTGCGTGGTGC
 TACTACCTCGACGAGTATGCCAGTACATCGAGAAGGATGCCGCTGGAGGCCGTTCCAGAAGGTGCTGGTGGACG
 AACCGAGCAGGAAGACACCATGCCATCTCCGTGGCCTCAAGGAACGCTATGAAGTGCACCAACGGGTGA

>ORF25892c (SEQ ID NO:292)

CCGCCTGGCCCAGCAGAAGGGCGACCAGTTCATCTCCAGCGAGCTGGTATTGCTGGCCGCGATGGACGAGAACACCAGGC
 TCGGCAAGCTGCTGCTCGGCCAGGGCGTGTGCGCAAGGGCTGGAGAATGCCGTGGCAACCTGGGTGGCGAACGG
 GTGAACGACCGAACGTCGAGGAGTCGCGCCAGGGCGTGGACAAGTACACCGTCGACATGACCAAGCGCGCAGGAAGG
 CAAGCTGACCCGGTGAATGGTCGCGACGAGATCCGCCGGACATCCAGGTCTGAGCGGACCAAGAACAAACC
 CGGTGCTGATGGCGAACCCGGCGTGGCAAGACCGCCATCTGAGGGCCTGGCCAGCGCATCATCAACGGCGAAGT
 CGGGACGGCTCAAGGACAAGCGCTGCTGGCCTGGACATGGGGGCGTGAATGGCGGTGCAAGTCCGGCGGAGTT
 CGAGGAACGCTGAAGCGGTCTCAACGAACTGGGCAAGCAGGAAGGCCGGTCACTCTGTCATCGACGAACTGCACA
 CCATGGTCGGCGCCGGCAAGCGGAAGGTGCCATGGACGCCAACATGCTCAAGCCGGCTGGCGCGGGAGCTG
 CACTGCGTCGGTGTACTACCCCTCGACGAGTATGCCAGTACATCGAGAAGGATGCCGCTGGAGGCCGTTCCAGAA
 GGTGCTGGTGGACGAAACCGAGCGAGGAAGACACCATGCCATCTCCGTGGCCTCAAGGAACGCTATGA

>ORF25110 (SEQ ID NO:294)

CGTTCTTGAGGCCACGGAGGATGGCGATGGTGTCTTCTCGCTGGTCTGCCACAGCACCTTCTGGAAAGCGCGCTC
 CAGCGCGCATCTTCGATGTACTGGCGATACTCGTCGAGGGTAGTAGCACCGACGCGAGCTCGCCGCGCGCCA
 GAGCCGGCTTGAGCATGGCCGGCTCCATGGCACCTTCCGCTTGGCGCCGCGACCATGGTGTGAGTCTGCGATG
 AACAGGATGACCCGGCTTCCCTGCTGGCCAGTTCTGAGGACCGCCTTCAGGCGTTCTGAACTCGCCGCGGAATT
 GGCACCGGGCGATCAGCGCCCCATGTCAGGGCCAGCAGGGCGTTGCTCTGAGGGCGTCCGGCACTTCGCGTTGATGA
 TGCGCTGGCCAGGCCCTCGACGATGGCGGTCTTGGCGACGCCGGGTTGCGCGATCAGCACCGGGTTGTTCTGGTCCGC
 CGCTGCAGGACCTGGATGGTCCGGCGATCTCGTCGCGACCGGATCACCGGGTCGAGCTTCCGCTTCCGGCGCGTT
 GGTCAATGTCGACGGTGTACTTGTCCAGCGCCTGGCGGACTCTCGACGTTGGTCTGGTCAACCGCTTGTGCTGAGCAG
 GGTTGGCCACGGCATTCTCAGCGCCTTGGCGACACGCCCTGGCGAGCAGCAGCTGGCGAGCCTGGTCTCGTCC
 ATCGCGGCCAGCAATACCGAGCTCGCTGGAGATGAACCTGGTGCCTTCTGCTGGGCCAGGCCGGTCAAGCCTGGTGTGAGCAG
 GCGTGCAGGATCTGGACAGGTTACGTCGCGGTGGCTCTGGATCTCGCGAGCGCGTCAAGTCTTGTGAGGAG
 CGCTGCAGGGCGGCGATATCGAAGCGCACCTGCACTGAGGGGCTGATCGAACCGCTTGTGCTGAGCAGGGCG
 GAAAGCAGGTGCACCGCGTCACTGGCGGATGGTCACTGGCCAACGCCAGGGACTGGCGTGGAGAGCGCAGTTGCAG
 CTTGCTGGTCAAACGGTCTATTGCACTGGTGTCTTCTATAGACGCGGCCGAAAGATGGGTGTCCCTGA

>ORF25510 (SEQ ID NO:296)

TGCGCTGGCCACGGCCCTCGACGATGGCGGTCTTGGCGACGCCGGTTGCGCGATCAGCACCGGGTTGTTCTGGTCCGC
 CGCTGCAGGACCTGGATGGTCCGGCGATCTCGTCGCGACCGGATCACCGGGTCGAGCTTCCGCTTCCGGCGCGTT
 GGTCAATGTCGACGGTGTACTTGTCCAGCGCCTGGCGGACTCTCGACGTTGGTCTGGTCAACCGCTTGTGCTGAGCAG
 GGTTGGCCACGGCATTCTCAGCGCCTTGGCGACACGCCCTGGCGAGCAGCAGCTGGCGAGCCTGGTCTCGTCC
 ATCGCGGCCAGCAATACCGAGCTCGCTGGAGATGA

>ORF26762c (SEQ ID NO:298)

CCGCCGACTGCCCTGCCGGCGTTGCTGCCGACCGCTCGGGCACCCGGGTGGCCGGGCCATGCCGGCTGGCGCGGGCTG
GCGGCGGGCGTGTGGAGGCAGCGTGGACAGCCTGGCGTGGCCGGCAGCAGACTGCTGGTCTGGCTGGGCGCGGCAT
CGGCCCCGAGGCCTTCGAGGTGGCGAGGTCCGCATGCATTCTCGCTGCCACGCCAGGGCGCTCGGCTTTCG
TACCTAGCGCCAATCCGGGCGCTTCATGGCCGACATCTACCGACTCGCGGGATCCGCTGGCGCCATGGCGTCACC
GCCGTGCAATGGCGGGCTTCTGCACCTTCAGCGATACCGCGCCTTCTATTCCCTACCGCCGCTCGTCGCGTACCGGGCCG
TTTGCCAGCTGGCTGGCTCCAGGACTAGGCCCGCGCAGGTTATCCGGCGCACTGACCGATGTCACGGTCCGGTCTG
CTTGAACCGCGGAAATGCCCTATCTACTGA

>ORF26257 (SEQ ID NO:300)

ATAAGGGCGATTCGCGGTTCAAGCGACGGGACCGTGACATCGGTAGTTGCCCGGATAACCTGCGCGGGCTAGT
CCTGGAGCCAGACCAGGCTGGAAAACGGCCGGTACGCGACGAGCGCGGTAGGAATAGAAGCGCGGTATCGCTGAAG
GTGCAGAACGCCGCCATGCACGGCGGTACGCCATGGCGCCAGCGGATCCGCGAGTCGGTAGATGTCGGCAT
GAAGCGGCCGGATTGGCGTAGGTACGAAAGCCGAGCGCCCTCGGGTGGCGAGCGACGAATGCATCGCGGACCTCGC
CGCCGACCTCGAAGGCTGCGGGCCGATCGCCGGCCCCAGCCAGACCAAGCAGTTCGTCGCCGGCACGCCAGGCTGTCC
ACCGTCGCCCTCCAGCACGCCGCCAGCCCGCCAGCGCATGGGCCGCCACCCGGGTGCCCGAGCGGTCGCA
GAACAACGCCGGCAGCGAGTCGGCGTATGATGTACAGGCAGCGCCGGCATCGCCTCCAGCTGGCGTCGGCCCTGCA
GCACCGTTCGGGTCCGCTCCACACGTACTCCGTGACCTATTCAACCAGCTCGGCCGCCATTCCAGACGCTCGGT
CAGGCCTCGCGGGTTTATTCCACGGCGCGGATCGTCGTAGACGTGGCGCCAAGGTTCAGACTGTCGAAGGGTGCCT
GGCTGA

>ORF26844c (SEQ ID NO:302)

CGTGGTGGAGGCCGACCGAACCGGTGCTAGGGCGACGCCAGCTGGAGCGCGATGCCGGCGTCGCCTGTACGATCAT
GACCGCCGACTGCCTGCGCGTGTGTCGACCGCTCGGGCACCGGGTGGCCGGCCCATGCCGGCTGGCGCGGGCG
TGGCGGGGGCGTGTGGAGGCACGGTGGACAGCCTGGCGTGGCCGGCACGAACCTGGCTGGCTGGGGCGGGCG
ATCGGCCCCCAGGCCCTCGAGGTGGCGAGGTCCCGATGCAATTGTCGCTGCCACGCCAGGGCGCGCTCGGCTTT
CGTACCTAGCGCAATCCGGGCCCTCATGCCGACATCTACCGACTCGCGCGGATCCGCCTGGCGGCCATGGCGTCA
CCGGCGTGCATGGCGCGCTCTGCACCTCAGCGATACCGCGCGCTTCTATTCTACCGCCGCTCGTGCCTGACCGGC
CGTTTGGCAGCCTGGCTGGCTCCAGGACTAG

>ORF26486 (SEQ ID NO:304)

ATGTCGGCCATGAAGCGCCGGATTGGCGCTAGGTACGAAAGCGAGCGCGCCTCGCGTGCAGCGACGAATGCATCGCGACCTCGCCGCCACCTCGAAGGCTCGGGCGATCGCCGGCCCAGCCAGACAGCAGTCGCGCCGGCACGCCAGCGCTGCCACCGCCAGCGGTCCACCGTCGCCCTCAGCACGCCGCCAGCCCCGCCAGCGCGCATGGGCCGCCACCCGGGTGCCAGGCCAGAACACGCCGCCAGGCAGTCGGCGGTATGATCGTACAGGCCACGCCGCCATCGCGCTCAGCTGGCTCGGCCCTGAGCACCGGTCGGGTCGCCCTCACCACGTCACTCCGTGCACCTATTCAACCAGCTGGCGGGCATTCAGACGCTCGGCTGGGTCAAGGTTAGACGTGGGCGCAAGGTTAGACGTGGGCGCCAGTGGGGTCAAGGGTGCCTGGCTGACCCGCCACTGCGCGTGGTCAGCAGGCCACACGCCGCCGGCGCCGGCCAGTCGGGGTCAAGGCCAGGGCTCAACCCAGCACCGCCAGTCGGGCGCAACAGGCTGAGCAGCCAGAGGAATTCTCCGGCAGCGGGATTCCCCACTTCATGCCACGCCGGTGGCCGGGTGA

>ORF26857c (SEQ ID NO:306)

GTGCACGGACTGACGTGGTGGAGGCCGACCCGAAACGGTGTCAAGGGCCGACGCCAGCTGGAGCGCGATGCCGGCGTCG
CCTGTACCATCATGACCGCCGACTGCCTGCCGGCGTTGTCTGCGACCGCTCGGGCACCCGGGTGGCCGCGGCCATGCC
GGCTGGCGCGGGCTGGCGGGCGGTGCTGGAGGCGACGGTGGACAGCCTGGCGTGGCCGGCGACGAACTGCTGGTCTG
GCTGGGGCCGGCATGGCCCGCAGGCTTCGAGGTGGCGAGGTCCCGGATGCATTGTCGCTGCGCACGCCGAGG
CGCGCTCGGTTTGTACCTAG

>ORF27314c (SEQ ID NO:308)

ACTGGGAATCGCCGCTGCCGAAGAATTCTCTGGCTGCTCAGCCTGTTGCCAGGATCGCAGGGTTCGTCGGTTGA
ACGCCCTGGCTGACCCCCGACTGGCCGGCGCCGCCGTGTGCGGGCTGCGTGACCAACGCGCAGTGGCGGGGTCA
GCACCCCTCGACAGTCTGAACCTTGGCGCCACGTCTACGACGATCCGCGCCTGGAATAAAACCGCCGACGCC
CGAGCGCTTGGAAATGCCGGCCGAGCTGGTTGGAATAGGTGCACTGGAGTGACGTGGAGGCCACCGAACCGGTG
CTCAAGGGCCGACGCCAGCTGGAGCGCGATGCCGGCGTCCCTGTACGATCATGA

Fig. 3-24

>ORF27730c (SEQ ID NO:310)

CAAGCCCGCCGGCCTGGTGGTCCATCCGGCTGCCGCCATCAGGACGGCACCCCTGCTGAATGCCTGCTTACCATGTCC
 CGGACATGCCAATGTGCCGCCGGATCGTCCACCGCCTGGACAAGGACACGCCGGCTGATGGTAGTGGCAAG
 ACGCTGGAGGCCACACCAAGCTGGTGGCGCAACTGCAGGCACGGTCGGCATCTACAGGGCGATCGTGTGATCGG
 CGTGTACCTCCGGCGGACCATCGATGCCGATCGGACGGCATGGCGTGCAGCGGAGAAGATGGCGGTGGTCAGG
 CGGCAAGGTGGCGGTAGCCATTACCGCGTGTGGAACGCCCTCCGTGCGCACACCCATACCCGGTCAAGCTGGAGAC
 GGGCGTACCCACCAAGATCCCGTGCACATGAGCCATATTGGCTATCCCGTGGCATCCGGTACCGTGGCGCTTCC
 CAGGATTCCCCCGGTGCCAGCCAGACCCCTGGTCCAGACTCTTCGCAATTCCCCCGGCAGGGCGTGCACCGCGCTTCC
 TCGAAGTGGATCACCCGGCACCCGGCGTGCATGAAGTGGATGCCGCTGCCGGAGAATTCTCTGGCTGCTCAGC
 CTGTTGCCAGGATCGCAGGGCGTGTGCGTGAACGCCCTGGCTGACCCCCGACTGGCCGGCGCCGGCGTGTGCGG
 GCCTGCGTGAACACCGCGCAGTGGCGGGGTAGCCAGGCACCCCTCGACAGTCTGAACCTTGGCGCCACGTCTACGACGA
 TCCCGCGCCGTGGAATAA

>ORF26983 (SEQ ID NO:312)

CCCCGCCACTGCGCGTGGTCACGCCAGGCCGACACGGGCCGGCGCCAGTCGGGGTCAGCCAGGCCGTTCAACCGA
 CGAACGCCCTCGCGATCTGGCGAACAGGCTGAGCAGCCAGAGGAATTCTTCGGCAGCGCGGATTCACCTCATGCGC
 ACGCCGGTGGCCGGGTATCCAGTCGAGGAAGCGCGGTGAGCGCCTGCCGGGGAAATCGCGAAGAGCTGGACAG
 GGTCTGGCTGGCCACCGGGGAATCTGAAGGCCACCGTAGACCGGATCGCCGACCAGGGGATAGCCAATATGGCTCA
 TGTGCACGCCGATCTGGTGGTACGCCGGTCTCCAGCTGACCCGGTATGGGTGTGCGCACCGGAAGCGTCCAGCACG
 CGGTAATGGCTGACCGCCACCTGCCGGCGTGCACCCGCATCTCTGCCGCTGCACGCCATGCCGTCCGATCGGCC
 ATCGATGGTGCCGCCGGATCACGCCGATCACGATGCCCTCGTAGATGCCGTCGACCGACCGTCCGTCAGTTGCG
 CCACCAAGCTTGGTGTGGGCTCCAGCTGGCCTTGGCCACTACCATCAGGCCGGTGTGTCCTTGTCCAGGCCGGGACATC
 CGGCCGCGGGCACATTGGCGATGTCGGGACATGGTAGAGCAAGGCATTAGCAGGGTGTGCCCTGTATGGCCGGCAGC
 CGGATGGACCACCAAGGCCGGCGGGCTGTCAATCACCAGGATGTGCTCGTCTCGTAGACGATTCCAGCTCGATGTCT
 GTGCGAGCCACTGCCCTGGCTTCCGTCGGCCTCCAGGACCAGTTGCGCGCCGTGTGGACGATGTGCGCGGGCAGC
 AGCACGGCGCCGTCACGGTCAGGCACCGTCTTGTACGCCGGCAGACGGAGGGAGTGTGCGGAAAAAGCTG
 GGCGCGATCTGGTCAGACGCTGGCCACCCAGCTGAACGGCACCTCGGCCGCGTGAATCATATCGGACATGAGTA
 G

>ORF28068c (SEQ ID NO:314)

CCACAGCGCGTAGCCGATTCCAAAAGCCGCGTGAACATCGTCTCTACTCATGTCGATATGATTCAACGCCGGCGA
 GGTGCCGTTGAGCTGGGTGGCCAGCGTCTCGACCAAGATGCCGCCAGCTTTTCCGAAACACTCCGCTCCGCTGG
 CGCGCTGGATCAAGGACGGTCCGCTGACCGTCGACGGCGCGTGTGCGCCCGCGACATCGCCACAGCGCGCGCAA
 CTGGCTCTGGAGGCCAGGAGGCCAGGAAAGCCCAGGGCGAGTGGCTCGACAGGACATCGAGCTGGAAATCGTCTACGAGGAGA
 GCACATCTGGTATTGACAAGGCCGCCCTGGTGGTCCATCGGCTGCCGGCATCAGGACGGCACCCCTGCTGAATG
 CCTTGCTCTACCATGTCGGACATCGCAATGTGCCGCCGGATCGTCCACCGCCTGGACAAGGACACGACCGGC
 CTGATGGTAGTGGCAAGACGCTGGAGGCCACACCAAGCTGGTGGCGCAACTGCAGGCACGGTCAAGCCATCTA
 CGAGGCGATCGTATCGCGTGTACACCTCCGGCGCACATCGATGCCGCGATCGGACGGCATGGCGTGCAGCGCAGA
 AGATGGCGTGGTGCACGCCGGCAAGGTGGCGTCAGCCATTACCGCGTGTGGAACGCTTCCGCGCACACCCATACC
 CGGGTCAAGCTGGAGACCGGGCGTACCCACCAAGATCGCGTGCACATGAGCCATATTGGCTATCCCGTGGCGATCC
 GGTCTACGGTGGCGCTTCAGGATTCCCCCGTGGCAGCCAGACCCCTGGTCCAGACTCTTCGCAATTCCCCCGCAGG
 CGCTGCACGCCGCGTCTCTCGAACCTGGATCACCCGGCACCGCGTGCACGAGTGGGAATGCCGCTGCCGGAAGAA
 TTCCCTCTGGCTGCTCAGCCTGTTGCGCCAGGATCGCGAGGCAGTGTGCGTGGTTGA

>ORF27522 (SEQ ID NO:316)

CCGACCGTGCCTGCAGTGGCGCCACAGCTTGGTGTGGGCCACTACCATCAGGCCGCTGGTCC
 TTGTCCAGGCCGGTGGACGATCCCGCGCGCGCACATTGGCGATGTCCGGACATGGTAGAGCAAGGCATTCA
 CGCGTCTGATGGCCGGCAGCCGGATGGACCAACAGGCCGGCGGGCTGTCAATCACCAAGGATGTGCTCCTCGT
 CGAATTCCAGCTCGATGTCTGTGCGAGCCACTGCCCTGGCTTCCGTCGGCCTCCAGGACAGTTGCGCGCCGCTG
 TGGACGATGTGCGCGCCGGCGCAGCACGGCGCGTCACGGTCAAGGACCGTCCCTGA

Fig. 3-25

>ORF28033c (SEQ ID NO:318)

GCATCGTCTCTACTCATGTCGATATGATTCAACGCGGCCGAGGTGCCGTTGAGCTGGGTGCCAGCGTCTCGACC
 AGATCGCCGCCAGCTTTCCCGAACACTCCCGTCCCGTGGCCGGCTGGATCAAGGACGGTCGCCTGACCGTCGAC
 GGCGCCGTGCTGCGCCCGCGACATCGTCCACAGCGCGCGCAACTGGTCTGGAGGCCGAGCAGGAAGCCCAGGGCGA
 GTGGCTCGCACAGGACATCGAGCTGAAATCGTACGAGGACGACATCCTGGTATTGA

>ORF29701c (SEQ ID NO:320)

TCTTCCAGTTCGCTGGAGATCAGCAGGACCACTACCGCCGATGGTCAGGCCGACAGGTGGTACAGACGGAGGATGCG
 TTGCCCCCTGCTCCTCGCTCAGCCGTAGCCGTTAGCGCGCACGGTCGCCCTGGCTGGCGACGGCCAAATGGCGCAGGGACCATCGCGATGC
 TACCAAGCGTGTGCTGGCGAGGGCGTTGGCTGGCGACGGCCAAATGGCGCAGGGACCATCGCGATGC
 GCTCGGCTCGTCTCGGCCAGTGGCTGGCGGGAGTGGGACGGGTAAGCGACGCCAGAGCGAACCGCGATGGCGA
 TCAGGGCGATCCAGAACAGGAGGCCAAAGGGCCATGGTATCTGGAGGCTGGAGAAAGCTGCAAGTTAGCCAAGCCG
 CCGGCTCGATCCCAGACGGGAAGGTCCAGGCTGTGGCGTTGGCGCTGGAGAGGCATGGCGCGGGCAAAAGAAGG
 GAGGCCCTGCCCTCCCTCGGTGTTCTGTGCGATCAGTCGAAGAGACCGAAGGTCACTGAGCTCCACCAAGGAGCGACCGG
 AGTCCTCGTCGTCATCGCTCCGGCTTCTCGTCGTCGGCGCTGTGATCCTGGTTTCCGGCTCAGTTCGGGGATC
 TCCCGCTCGGATCCTCGTACTGCTTGTACCGTCTGGCGGCCAGCCAGGAGCGGGTGTGGCGCTCGCTTCGGGGCGACGAACCTGCCATCCTGA
 GATCAGGCCAGGGTGGCTTGGCCAGCCAGGAGCGGGTGTGGCGCTCGCTTCGGGGCGACGAACCTGCCATCCTGA
 GGCTGGCGTATCCGGATAGTTCAGCTTGAGGGTTTCCAGGCTGGTGTGGCCAGGTGTCGAGACCCAGGCAGGGTAG
 GCTTCGACCATGATCGCCAGGCCATGCCGACGGCCGGGTTTCCCTGGAAAGTCTCCACACGTAGCGACCGCGGTTGGC
 GGCAGCGACATAGGCCTGGCGCTTCAGGTAGTGTGGCCAGTCAGTCCGAGGCTGGCGACAGGTTGCGCAGGTACA
 CCATGCGCCTTGGCGTCCGGGCGTAGCGGTGTTGGGAAGCGGTGGTGAGCTGGCGAAGTGTGAAGGAGTCG
 CGGGCGGCCGGGTCGCGTTGGTATGTCAGCGGAGGAGCGGGCCAGGAGCGGGCTGGTCAAGGAGGA
 CAGGCCCTTGAGGTAGTGGCGTAGTCGACGTTGGGTGTGGCGATGAGCGGGATGAAGCGTTCGGCGGGCGCGGG
 CGGCTCAGGGCTCCATGTTCTGTAGTGGCGTAGATCAGTCGAGCTGGGCTGTCGGCGTAGCGGCCAGGGAGTAG
 CGCGATTGAGGGCTTCAGCTGGTACGGCGCTGTTGTAAGCTCTTGTGTTGGCGTAGCTGGCGCTGTCGCGTAG
 CTGGCTCTCGCTCAGGTCTCGTCGACAGTCTCTTGTGAGGAGCAGGCTGCGGTGAGGGAGGATGGCGATCAGCA
 GCAGGTGTTCACTTGCATGGCGCTTGCCTGGCGCTGGGACGGTGGCTGGCCTCAACCGTCTGTTATGA

>ORF28118 (SEQ ID NO:322)

CAGACGGTTGAGGCCAAGCGACCGTCCAGGGACGCAAGCGCCATGCAAGTGAACACCTGCTGCTGATCGCCATCCT
 CGCCCTCACCGCAGCCTGCTCCTCGAACAAAGGAGACTGTCGACGAGAACCTGAGCGAGAGGCCAGCTGTACCGAGGCC
 AGGACGACCTCAACAACAAGAGCTACAACAGCGCCGTACCAAGCTGAAAGCCCTCGAATCGCGCTATCCCTCGGCC
 TACGCCGAGCAGGCCAGCTCGAGCTGATCTACGCCAACACTACAAGAACATGGAGGCCAGGCCGCGCTGGTCAAGGAGGA
 ACGCTTCATCCGCTGCATCCGAGCACCCAAACGTCGACTACGCCACTACCTCAAAGGCTGTCCTCCCTCGACCAAGG
 ACCCGCCGCTGCTGGCGCTTCTGCCGTGGACATGACCAAGCGGCCAGCCGGCGCCGCGACTCCTCAACGAG
 TTCGCCAGCTCACCGCGTCTCCCAACAGCGCTACGCCCGACGCCAGGGCGCATGGTGTACCTGCGCAACCT
 GCTGGCGGCCCTACGAAGTGCACGTCGGCCACTACTACCTGAAGGCCAGGCCATGTCGCCGCCAACCGCGTCGCT
 ACGTGGTGGAGAACTTCCAGGAAACCCCGGCCGTCGGCGATGGCTGGCGATGGTCAAGGCTACCGTGCCTGGGT
 CTCGACGACCTGGCCAGCACCAGCCTGGAAACCCCTCAAGCTGAAACTATCCGGATAACGCCAGCTCAAGGATGGCGAGTT
 CGTCGCCCGCAAAGCGAGGCCACCCGCTCTGGCTGGCAAGGCCACCCCTGGCGTGTGAAGGCCAGGCC
 CGCCGCACATGGAAACCCAGGCCACAGGACGTGATCAAGCAGTACGAGGATGCCAGCGGCCAGGAGATCCCCGCC
 AACTGAGCGAAAACCAGGATCACAGCGCCGACGAGAAGCGGAGAGCGATGACGACGAGGACTCCGGCTCCTGGT
 GAGCTACATGACCTCGGTCTTCGACTGA

>ORF28129 (SEQ ID NO:324)

GGCCAAGCCGACCGTCCAGGGACGCAAGCGCCATGCAAGTGAACACCTGCTGCTGATGCCATCCTGCCCTCACCG
 CAGCCCTGCTCCTCGAACAAAGGAGACTGTCGACGAGAACCTGAGCGAGAGGCCAGCTGTACCGAGGCCAGGCC
 AACAAACAAGAGCTACAACAGCGCCGTACCAAGCTGAAAGCCCTCGAATCGCGCTATCCCTCGGCCGCTACGCCGAGCA
 GGCCAGCTCGAGCTGATCTACGCCAACACTACAAGAACATGGAGGCCAGGCCGCGCCGCCAACGCTTCATCC
 GCCTGCATCCGAGCACCCAAACGTCGACTACGCCACTACCTCAAAGGCCATGCCCTCCGACCAAGGACGCC
 CTGGCGCTTCCCTGCCGTGGACATGACCAAGCGGCCAGCCGGCGCCGACTCCTCAACGAGTTCGCCAGCT
 CACCAGCCCTTCCCAACAGCGCTACGCCCGACGCCAAGGCGCGCATGGTGTACCTGCGCAACCTGCTGGCGCCT
 ACGAAGTGCACGTCGGCCACTACTACCTGAAGCGCCAGGCCATGTCGCCGCCAACCGCGGTGCTACGTGGTGGAG
 AACTTCCAGGAAACCCCGGCCGTCGGCGATGCCCTGGCGATCATGGTCAAGCCTACCGTGCCTGGGTCTCGACGACCT
 GGCCAGCACCAGCCTGAAACCCCTCAAGCTGAACATCCGGATAA

>ORF29709c (SEQ ID NO:326)

GGACCTGATCTTCCAGTCGCTGGAGATCAGCAGGACCACTACCAAGCCGATGGTCAGGGGTACAGGTGGTACAGACGG
 AGGATGCGTTGCCCTGCTCCTCGCTCAGCCGTAGCCGTTAGCGCGCACGGTCGCCCTGGTCTGGCGCAGGTGCGCCT
 GGCTGCAATACCAGCGTTGTTCTGGGGCGAGGGCGTTGGCCTGGCGCACGTGGACGCCAATGGGCGCAGGGACCCATC
 GCGATGCGCTCGGCTCGCCTGGACGTTGCTGGCGGGAGTGGGACGGTAAAGCGACGCCAGAGCCAGAACGC
 GATGGCGATCAGGGCGATCCAGAACAGGAGGGCGAAAAGGCCATGGTATCTGGAGGCTGGAGAAAGCTGAGTTAG
 CCAAGCCGGCGCTCGATCCCAGACGGGAAGGTCCAGGCTGTGGCGCTGGGAGAGGCATGGCGGGCAA
 AAAGAAGGGAGGCCTGCGCCTCCCTCGGTGTTGCGATCAGTCGAAGAGACCGAAGGTATGTAG

>ORF29189 (SEQ ID NO:328)

TCGCACGAAACACCGAAGGGAGGGCGAGGCCTCCCTCTTTGCCCCGCCATGCCCTCTCCAGCGCCAAACGCCGCA
 CAGCCTGGACCTCCCGTCTGGATCGAGCCGGCTTGGCTAAACTGCAGCTTCTCCAGCCTCGAGATCACCAG
 GCCTTTCCGCTCCTGTTCTGGATCGCCCTGATCGCATCGCTCTGGCTCTGGCTCGCTTACCCGCTCCACTCC
 CGCCAGCAGAACGTCCGAGGACGAGCCGAGCGCATGCCGATGGTCCGCTGCCATTGCGCGTCCACGTGCCGCA
 GGCAACGCCCTGCCAACGAACAACGCTGGTATTGAGCCAGGCGACCTGCGCCAGGACCAGGGGACCGTGC
 GCGCTGA

>ORF29382 (SEQ ID NO:330)

TCGCCATCGCTCTGGCTCGCTTACCGTCCACTCCGCGCAGCAGCAACGTCCGAGGACGAGCCGAGC
 GCATCGCCGATGGTCCGCTGCCATTGGCGCTCACGTGCCAGGCCAACGCCCTGCCACGAACACGCTGGTA
 TTGCAAGCCAGGCGCACCTGCCAGGACCAAGGGCGACCGTGCCTGACCGTACGGCTACTGGTCTGATCT
 CAGCAGGCTGAGGAGGAGCAGGCCATCGCTCTGGTACTGGTCTGACCTGGTCTTACATCTGGTCT
 TCAGGTCTCAAGCTCGTCCACCGTAACTGTCCATGTCGGCAGTGGTCTGACCTGGTCTTACATCTGGTCT
 TGTTCTGCCGCGTGCAGCAATTGCTGCCGATCTCATCTCGCGCTCACCGACGTGCTGATGCTTGC
 GCCTGGCGCTGTCATCCGCGCCATTGCAACATCTGCTGCCGCG
 GCATCGCCCTGGTCACTGCCGGCGGCCAGCCTGCCGCTGCTCACCTGACCTCTTCCTCAGCCTGAGCAGTCCGG
 ACGCCACCAACCACTACGTCCAGGCCGGGGCCTGGCACCCCTGTGCTTCGCCGCGCTGGTATCCAGGCTCTGGT
 CGGCCAGGAGCAGACCGAAACGCTGGCGAAGAACGCCGAGACGGTGCACCTGGAGGAACCTAACGCTATTGAT
 CCTGCAGCGCATGCCACGGCATTCTCGTGGCTAGCCGTCAGGCCATCTCCGCCAACAGGCCCTCGCC
 TGCTCAGGCGAGGACGACGTGCAGGGCGCCAGCCTGCCACAGCCGATGCTGATGCACTGCAAGCAATGGCG
 CTGAATCCAGCCTCCGCGCCAGCTCAAGGTGGTGCAGGCGATGGCCGACGGTCAACCCAGCTTATGCC
 CCGCGAAGACGACCAGCACGTGCTGATCTTCCTCGAAGACATTGCAAGATGCCAGCAGGCCAGCAGATGAAGCTGG
 CGCGTCTGGCGCCTGACGCCGGCATGCCATTGAGATGCCAACCCGCTGGCGCATGCCACGCC
 CTGCAAGGAGTCAGAGGAACGGATGCCCGGACGCCGACGCCGACGCAAGTCACTCAGGACCACTGCAAGCG
 GATGAACTGGTCTGCAAGCTCTCCGCTGCCGCCAGGCCAACCGCAGCAGCTCGACCTGCAAGGAGTGGCTTCAGC
 GGTCATCGAGAACGCTCTGCAAGCTCTCCGCTGCCGCCAGGCCAACCGCAGCAGCTCGACCTGCAAGGAGTGGCTTCAGC
 CGCATGGACCCACACCAGTTGAACCAAGGTGCTGAGCAACCTGGTGCAGAACGGTCTCGTACAGGCCAGGCCAGCG
 GCGCGGCCAGGTCTGGCTGAGCCTGCCGCGACCCGGAGAGCGACCTGCCGCTGGTGAAGTCATGACGACGGTCCCG
 GCGTACCGCGGACAAACTGAACAAACCTGTTGAACCCCTTTACTACAGAAAGCAAGGCACCGCCTGGCCTCTAT
 CTCTCCCGCGAACTCTGCGAGAGCAACCAGGCACGGTCACTACCGCAATCGCGAGGAAGGCCGCGCTGCTTCCGCA
 CACCTCGCCACCCCGCAGAACCTCAGCTGA

Fig. 3-27

>ORF30590c (SEQ ID NO:332)

CTCCTGCAGCAGTTGGCGGCGTGGCTGATCGCGCCAGCGGGTTGCGGATCTCATGGCGATGCCGGCGGTCAAGCGGC
 CAAGACCGCCAGCTTCATCTGCTGCCCTGCTGGCGATCTGCAGAAATGCTTCGAGGAAGATCAGCACGTGCTGGTC
 TCTTCGCGGTTGAGGCTGATAAAAGCTGGGTTGACCGTCGGGCCATCCGGCACCACTTGAGGCTCGGCGGACGGAGGCT
 GGGATTCAAGGCGCCATTGCTCATGCAGTGCATCAGCATCGGGCTGTGGCGGCGAGGCTGGGCCCTGCACGTGCTCCT
 GCCTGAGCAGGCCAGGGCGGGCTGGTGGCGAGGAGATGGCTGACGGCTATCGACCACGAGGATGCCGGTGCATG
 CGCTGAGGATCAATGCGTTGAGTTCCTCCAGGTTGGCGACCGTCTCGGCGGTTCTCGGCCAGCGTTGGTCTGCTC
 CTGGCGCCGCACCAGAGCCTGGATCACCAGCGCGGCCGAAAGCACAGGTGCCAGGCCGGCTGGACGTAGTGGT
 TGGTGGCGTCCGGACTGCTCAGGCTGAGGAAGAGTCAGGTAGAGCAGGCCAGGCTGGCCGCCGCGATGACCAAGG
 CCGATGCGCCCGCGCAGCAGGATGTTGGCAATGGCCACCGCCACCAAGCAGGCTGCCATGCCGTGGTACGCCGCC
 ACCTGCGTAGAACAGGCCGAAAGCATCAGCACGTGGTGAAGACCAGGTAGCACCAACTGCCACATGGAACAGTTCAGGGTGGACGAGCTTG
 GCAGGAACAGCGCAGGCCGAGGATGTTGAAGACCAGGTAGCACCAACTGCCACATGGAACAGTTCAGGGTGGACGAGCTTG
 AGGACCTGATCTCCAGTCGCTGGAGATCAGCAGGACCACTGAGGCCATGGTCAGGCCGTACAGGTGGTACAGACG
 GAGGATGCGTTGCCCTGCTCCTCGCTCAGCCGTAG

>ORF29729 (SEQ ID NO:334)

ACTGTTCCATGTCGGCAGTTGGTCTACCTGGCTTCAACATCCTGGTGGCTGTTCTGCCCGTGGCGCAATTGC
 TGCGATCTTCATCCTCGCGCTACCGACGTGCTGATGTTGCGGCTGTTCTACGCAAGGTGGCGGCTACCCAGCGGC
 ATCGGCAGCCTGCTGGTGGTGGCGTGGCCATTGCCAACATCCTGCTGCGCGGCCATGGCTGGTCATCGCGGCC
 GGCGCAGCCTCGGCCTGCTCACCTGACCTTCTCCCTAGCCTGAGCAGTCCGACGCCACCAACCACATGTCAGGCC
 GCAGGCTCGGCACCCCTGCTTCGCCGCCGCTGGTGAATCCAGGCTGGTGCAGGCCAGGAGCAGACCGAAACGCTG
 GCCGAAGAACGCGCCGAGACGGTCGCCAACCTGGAGGAACCTAACGCAATTGATCCTGCAGCGCATGCGCACCGC
 ATCCTCGTGGTCGATAG

>ORF30221 (SEQ ID NO:336)

CCGTCAGGCCATCCTCTGCCAACCAGGCCGCCCTGGCCTGCTCAGGCAGGACAGTGCAGGGGCCAGCCTCGGCC
 GCCACAGCCCAGTGTGATGCACTGCATGAAGCAATGGCGCTGAATCCAGCCTCCGCGCAGCCTCAAGGTGGTG
 CCGGATGGCCGACGGTGCACCCAGCTTATCAGCCTAACCGCAAGACGACCAGCAGTGTGATCTTCCTCGAAGA
 CATTTCGAGATGCCAGCAGGCCAGCAGATGAAGCTGGCCGGTCTGGCGCCTGACCGCCGGCATGCCCATGA

>ORF30736c (SEQ ID NO:338)

AGCCACTCCTCAGTCGAGCTGCTGCCCTGGCCTGGCGCAGGGAGAGCTGCAAGGACGTTCTCGATGACCAAGTT
 CATCCGCTTCGACTGGCTCTGGATGATCTGCGTCAGGCGTGGTCCGGGCATCCAGTTCTGACTCCTGAGCAGTT
 GGGCGCGTGGCTGATCGGCCAGCGGGTGGCGATCTCATGGCGATGCCGGGTCAAGGGCCAAGACCGGCCAGC
 TTCATCTGCTGCCCTGCTGGCGATCTGCGAAATGCTTCGAGGAAGATCAGCACGTGCTGGTGTCTCGGGTTGAG
 GCTGATAAAAGCTGGTGTGACCGTCGGGCCATCCGGCACCACTTGAGCGTGGCGGACGGAGGCTGGGATTCAAGCGCC
 ATTGCTTATGCACTGCAGTGCATCAGCATCGGGCTGTGGCGGCCAGGCTGGCGCCCTGCACGTGCTCTGAGCAGGCC
 AGGGCGCTGGTGGCGAGGAGGATGGCCTGA

>ORF30539 (SEQ ID NO:340)

GATCCGCAACCGCTGGCGGATCAGCCACGCCAACACTGCTGCAGGAGTCAGAGGAACGGATGCCCGGACCGAC
 GCCTGACGCACTGCAGATCATCCAGGACCACTGCAAGCGGATGAAACCTGGTCATCGAGAACGTCCTGCAGCTCTCCGCTGCC
 CAGGCCAACCGCAGCAGCTGACTGAAGGAGTGGCTCAGCGGTCAGCAATCCAGACCCGATGGACCCACCCAGTTGAAC
 CAGCCAATGCACTGCAGCTCGGTGCCGGCAGATCCAGACCCGATGGACCCACCCAGTTGAACCAAGGTGCTGAGCA
 ACCTGGTGCAGAACGGTCTTCGCTACAGCGCCAGGCCAGGGCGCAGGGCGCCAGGCTGGCTGAGCCTGCCGCC
 GAGAGCGACCTGCCGTGGAGGTCATCGACGACGGTCCCGCGTACCGGGACAAACTGAACAAACCTGTTGAAC
 CTTCTTAACTACAGAAAGCAAGGCCACCGGCCCTGGGCCTCTATCTCTCCCGCAACTCTGCAAGAGCAAC
 CAGCTGACCGCAATCGCGAGGAAGGCCGGCGTGTCTCCGATCACCTGCCACCCCGCAACTCAGCTGACGGAA
 CGCGACCGCATGAGGCCGACAAAAGCCCTGATCGTCGACGATGAACCGATATCCGCAACTGCTGGAAATCA
 CTCACCGACATGCGCTGCCGGACGGCAGCGGCCCTGATCTGGTCCAGTACATCCAGCAGCGCATCCACAGAC
 CGGCCATGA

Fig. 3-28

>ORF31247c (SEQ ID NO:342)

TTTCCAGCAGTCGGGATATCCGTTCATCGTCGACGATCAGGGCTTTGTCGGCTCATCGTCGGCTCCGTCAGC
TGAGTTTGCAGGGGGGGCGAAGGTATGCGAAGCAGCCGCCCTCCTCGGATTGCGGTAGTCGATCCGTCCTGG
TTGCTCTCGCAGAGTCGGGGAGAGATAGAGGCCAGGCCGGTGCCTTGCTTCTGTAGTAAAGAAGGGTTCGAACAG
GTTGTTCACTTTGTCGCCGGTACGCCGGGACCGTCGTGACTGACTTCCAGCACCCGAGTCGCTCTCCGGTCCGG
CGAGGCTAGCCAGACCTGGCCGCCGGTGCCTGGCGCTGTAGCGAAGACCGTTCTGCACCAGGTTGCTCAGCAC
TGGTCACTGGTGGGTCCATGCCGGTCTGGATGTCGCCGGCACCGAGCTGCAGGTGCAGTTGGCTGTCGTTGCGCAG
CCTGCCGGGTATTGTCGACGAACCGCTGAAGCCACTCTCAGGTCGAGCTGCTGCCGGTCCGGCTGGCGCAGGG
AGAGCTGAGGACGTTCTCGATGACCAGGTTCATCCGCTCGACTGGCTGGATGATCTGCGTCAGGCGTCGGTCCGG
GCATCCAGTCCTCTGA

>ORF30963c (SEQ ID NO:344)

CTTCCAGCAGGGCAGGTGCGCTCTGGGTCGCGCGAGGCTAGCCAGACCTGGCCGCGCCCGTGCCTGGCGCTG
TAGCGAAGACCGTTCTGCACCAAGGTTGCTAGCACCTGGTCAACTGGTGTGGGTCCATGCGGGCTGGATGTCGCCGGC
ACCGAGCTGCAGGTGCAAGTGGCTGTCGTCGAGCCTGCCGGGTATTGTCGACGAACCGCTGAAGCCACTCCTCA
GGTCGAGCTGCTGCGGTTGGGCTGGCGAGGGAGAGGCTGCAGGACGTTCTCGATGA

>ORF31539c (SEQ ID NO:346)

GGCGGGTGGCCACCGCTCCCGCAAGCGACCGAGGTCGACCGGTTGGTGAGGAAGTCGAAGGCACCGGCTTGAGCGCCTGGATCGGGTGTCCAGGCTGCCGTACCGGGTGTACATGGCCACCGGGCTGTGGATGGCGCTGCTGGATGTACTGGACCAAGATCGAGGCCGCTGCCGTCCGGCAGGCGCATGTCGGTGAGGCACAGGTCGAACGGCTCGCGGGCCAGCAACTCGCGGCTTCCCTTGACGTTGGGGCTGGGGTGTCCAGCTTATGCGGCCAGAGTGATTTCAGCAGTTGCGGATATCCGGTTCATCGTCGACGATCAGGGTTTTTGTGCGCTCATGCGTGCCTCCGTCAGCTGA

>ORF31222 (SEQ ID NO:348)

ACCGGATATCCGCGAAGTGGAAATCACTCTGGCCGCATGAAGCTGGACACCCGCAGCGCCCGCAACGTCAGAGGA
CCCGCAGTTGCTGGCCCGCAGCGCTTCGACCTGTGCCTACCGACATGCGCCTGCCGACGGCAGGGCTCGATCTGG
TCCAGTACATCCAGCGCCATCCACAGACCCGGTGGCATGATCACCGCTACGGCAGCCTGGACACCGCAGTCAG
GCCGCTCAAGGCCGGTGCCTCGACTTCCTCACAAACCGGTGCGACCTCGGTGCGCTGCCGGAGCTGGTGGCAACCGCC
ACGCTTGCAGCAACCGGAAGCGAGGAAGCGCCGGTGGACAACCGCTGCTGGCAGTCGCCGCGATGCGCAGCC
GCAACCAAGATCGGCAAGCTGGCGCAGCCAGGCGCCGGTACATCAGTGGCAGTCGCCGAGCGGCAAGGA
GCGCGCTGATCCACCGAGCAGGGCACGTATCGAGCGGCCGTTGCGCGTGAAGTGCAGGCGCAGTCAGGCG
GATGGAAAGCGAGTTCTCGGCCACAAGAAAGGCAGCTTCACTGGCGTATCGAAAGACAAGCAGGGCTGTCAGGCC
CCAGCGGTGGCACCCCTGTTCTCGACGAAGTCGCCGACCTGCCGATGCCATGCAAGTCAAACGTC
GAAAGGCCGTGCGCGGGTGGCGGCCAGCAGGAGGTGCGCGTGCACGTGCGCATCCTCTGCCACCCACAAGGACC
TCGCCCGAAGTCGGCGCCGGCGCTCCGCCAGGACCTCTACTACCGCTCAACGTATCGAGCTGCCGTAACCCG
TGCAGCAACGCCGAGGACATCCGCTGCTGCCGAACGATCCTCAAGCGCTGCCGACACCGGCTGCCGCC
GCCAGGCTGACCGGCACGACAGGAGAAGCTGAAGAACTACCGCTCCGCCGACGTCCGAGCTGGAAA
GGAGCGCCCTATACCGTGCAGAGACGACAGATCCAGCCTACGACCTGCCGATGCCGAGCTGGCAGGCC
AGGAAGGCCGCGAGCTGAGCGAAATCGACAACCTGAGGACTACCTGGAAAGACATCGAGCGCAAGCTGATCATGCAG
GCACTCGAGGAGACCCGCTGGAAACCGCACCGCCGGCCAGCGCCTGGCCTGAGCTCCGCTGATGCC
GAAAGCTGGGATCGACTGA

Fig. 3-29

>ORF31266 (SEQ ID NO:350)

AGCTGGACACCCGCAAGCAGCGCCGCAACGTCAAGGAAGCCGAGTTGCTGGCCCGAGCCGTTGACCTGTGCCTCACCG
 ACATGCGCTGCGGACGGCAGCGCCTGATCTGGTCCAGTACATCCAGCAGCGCATCCACAGACCCGGTGGCCATG
 ATCACCGCGTACGGCAGCCTGGACACCGCGATCCAGGCGCTCAAGGCGGTGCGCTCGACTTCCTCACCAAACCGGTCGA
 CCTCGGTGCGCTTGCAGGGAGCTGGTGGCAACCGCCCTACGCTTGCAGCAACCCGGAAGCCGAGGAAGCGCCGGTGGACAACC
 CCTCGGTGCGCTTGCAGGGAGCTGGTGGCAACCGCCCTACGCTTGCAGCAACCCGGAAGCCGAGGAAGCGCCGGTGGACAACC
 ATCAGTGGCGAGTCCGGCAGCGCAAGGAACCTGGTGGCGCCTGATCACGAGCAGGGGCCACGTATCGAGCGGCGTT
 CGTGGCGGTGAACCTGCGGCGGATTCCTCCGAGCTGATGAAAGCGAGTCTCGGCCACAAGAAAGGCAGCTTCACTG
 GCGCTATCGAAGACAAGCAGGGCTGTTCCAGGCCAGCGTGGCACCCGTTCTGACGAAGTCGCCACCTGCC
 ATGGCCATGCGAGTCAAACGTCTGGCGATCCAGGAAAAGCCGTGCGCGGTCGGCGGCCAGCAGGAGGTGCGCGT
 CGCACGTGCGCATCCCTGCGCCACCCACAAGGACCTCGCGCGAAGTCGGCGCCGGCGCTTCCGCCAGGACCTCTAC
 TACCGCCTCAAGTCATCGAGCTGCGCGTACACCGCTGCGCAACGCCGAGGACATCCCGTCTCGCCGAACGATC
 CTCAGCGCTGGCGGACACCGGCTGCGCCAGGCTGACCGGAGCCACAGGAGAAGCTGAAGAAACTACCG
 CTTCCCGGCAACGTCCGAGCTGAAACATGCTGGAGCGCCTATACCGTGTGCGAAGGACCGACAGATCCAGCCTC
 ACGACCTGCGCTGGCGATGCGCGGGTGCAGGCCAGGAAGGCGCCGAGGCTGAGCGAAATCGACAACCTCGAGGAC
 TACCTGGAAAGACATCGAGCGCAAGTGTATCATGCGAGGACTCGAGGAGACCGCTGGAACCGCACCGCGGGCCAGCG
 CCTGGGCTGACGTTCCGCTGATGCGTACCGCCTGAAAGCTGGGATCGACTGAAAGTGAAGAAGGCTGTCCGAAG
 ACAGGCCCTTGGTTTCGCTCAGAGGCAGGCCAGCGGGCTAGGGGCGGTAGGGGCGGGTCAAGCGTGA

>ORF31661c (SEQ ID NO:352)

ACCGGGCGCTGGCTGCGGCCAGCTGGTGCAGGGCGCGATCGGCCGAGCTGCCGAGCAGGGCGTT
 GTCCACCGGGCCTTCCTCGGCTTCCGGTTGCGCAAGCGTAGGGCGGTGCCACCGCTCCGCAAGCGACCGAGGTCGA
 CCGGTTGGTGGAGGAAGTCGAAGGCACCGGCTTGAGCGCTGGATCGCGGTGTCAGGCTGCGTACCGGTGATCATG
 GCCACCGGGGCTGTGGATGGCGCTGCTGGATGTAAGGACAGATCGAGGCCGCTGCCGTCCGGCAGGCCATGCGGT
 GAGGCACAGGTGCAACGGCTGCGGGCCAGCAACTCGCGCTTGA

>ORF32061c (SEQ ID NO:354)

AGGTCTGGCGGAAGGCCCGGCCGACTTCGGCGAGGTCTTGTGGGTGGCGCAGAGGATGCGCACGTGCGACGG
 CGACCTCTGCTGGCCCGACCGCGCGACGGCTTTCTGGATCGCCGGAGCAGTTGACCTGCATGCCATCGGC
 AGGTGGCGACTTCGTCGAGGAACAGGTGCCACCGCTGGCGGCTGGAACAGGCCCTGCTTGTCTCGATAGCGCCAGT
 GAAAGCTGCTTCTGTGGCGAAGAACTCGCTTCCATCAGCTGGAGGGAAATCGCCCGCAGTTCACCGCAGAAC
 GCCGCTCGATACTGGCCCTGCTCGTGGATCAGCGCGCACCAAGTCTTGCCTGCCGACTGCCACTGATGTAG
 ACCGGCGCTGGCTGCGGCCAGCTGGTGCAGGGCGCATCGGCCGACTCGCCGAGCAGGCCGTT
 GTCCACCGGGCCTTCCTCGGCTTCCGGGTGCGCAAGCGTAG

>ORF32072c (SEQ ID NO:356)

GGCGGTAGTAGAGGTCTGGCGGAAGCGCCCGGCCGACTTCGGCGAGGTCTTGTGGGTGGCCAGAGGATGCGC
 ACGTGCACGGCGACCTCTGCTGGCCCGACCGCGCGACGGCTTTCTGGATCGCCGGAGCAGTTGACCTGCA
 TGGCCATCGGCAAGGTGGCGACTTCGTCGAGGAACAGGGTGCCACCGCTGGCGGCTGGAACAGGCCCTGCTTGTCTCG
 ATAGCGCCAGTGAAGCTGCTTCTGTGGCGAAGAACTCGCTTCCATCAGCTGGAGGGAAATCGCCCGCAGTTCA
 CGGCACGAACGGCCGCTCGATACTGGCCCTGCTCGTGGATCAGCGCGCACCAAGTCTTGCCTGCCGACTCGC
 CACTGATGTAG

>ORF31784 (SEQ ID NO:358)

TGGAAAGCGAGTCTCGGCCACAAGAAAGCAGCTTCACTGGCGTATCGAAGACAAGCAGGGCTGTTCCAGGCC
 AGCGGTGGACCCCTGTCCTCGACGAAGTCGCGCACCTGCGATGGCATGCAGGTCAAACACTGCTCCGGGCGATCCAGGA
 AAAGGCCGTGCGCGGTCGGCGGGCAGCAGGAGGTGCGCGTGCACGTGCGCATCTCTGCGCCACCCACAAGGACCTC
 GCCGCCGAAGTCGGCGCCGGCGCTTCCGCCAGGACCTCTACTACCGCCTCAACGTATCGAGCTGCGCGTACACCGCTG
 CGCGAACGCCGAGGACATCCGCTGCTCGCGAACGCACTCTCAAGCGCCTGGCGGCCACCCGGCTGCCGCG
 CAGGCTGA

Fig. 3-30

>ORF32568c (SEQ ID NO:360)

GGAGCGAAAACCAAAGGCCTGTCCTCGGACAGGCCTTCACTTCAAGTCATGCCAGCTTTCAAGGCCTAGCGA
 TCGAGCGGAACGTCAGGCCAGGCCTGGCCGGCGGTGCGGTTCCAGCGGGTCTCCTCGAGTCGCTGCATGATCAGC
 TTGCGCTCGATGTCCTCCAGGTAGTCCTCGAGGTTGTCGATTCGCTCAGGCTCGCGCCTTCCTGGCTGGCACCCGG
 CGCATCGGCCAGGCAGGCTGAGGCTGGATCTGGCTTCGACAGGGTATAGGCGCCTCCAGCATGTTTCCA
 GTCGCGGAGCTGCCCCGGAGCGGTAGTTCTCAGCTCTCCTGCGTCGCCCCGTCAGCTGGCGCCGGCAGGCCG
 GTGTCGCCGCCAGGCCTGAGGATGCGTCGGCGAGCAGGGATGTCCTCGCCGCTTCGCGCAGCGGTGTACGCGC
 AGCTCGATGACGTTGAGGCCGTAG

>ORF33157c (SEQ ID NO:362)

ACAGACGGAGGTGCGCGGCTGGTTCGCGACGGCGATCGAGTGGTCGGGTGGCGACCTCGCGTGGCGAGATCCGTGGCG
 ACAAGGTGCTGCTGGCGCAGGCCCTGGAGCGCGAGTTGTAAGCGCTTGGCCTGGAACCTGCCCCTGGTACCGGTG
 AAAGGTCAAGATGATCCTCTACAAGTGCAGGGCGGATTTCTGCGCGCATGGTGTGGCCAAGGGCGCTACCGGATTCC
 GCGCGCACGGCCACATCCTGATCGGCAGCACCTGGAACATTGCGCTTCGACAAGACGCCGACGAGCGCTGG
 AAAGCCTCAGGGCGTCTGCGGAGAACTGTTGCGGAACCTGGCGACATGCAAGCGGGTGGCCACTGGGAGGGTTGCGC
 CCGGGCTCTCCGAAGGCATCCCCATATCGTCCGGTGCCTGGCTTCGACGGGCTCTGGCTGAATACCGGGCACTACCG
 CAACGGGTGGTCTGGCACCGCGTGTGCGCTGCTGGGGATCTCATGAGCGGGGGGAAACCGATCATCGACCCGG
 CCCCCCTACGCCCGGCTGGTCCTGAGGAGCGAAACCAAAAGGCTGTCTCGGACAGGCCCTTTCACTTTCAGTC
 GATGCCAGCTTTCAAGCGGTAGCGCATCGAGCGAACGTCAGGCCAGGCCTGGGCCGGTGCAGGTTCCAGC
 GGGTCTCTCGAGTGCCTGCATGA

>ORF32530 (SEQ ID NO:364)

AAAGGCCTGCGAAGACAGGCCTTGGTTTCGCTCCTCAGAGGCACCAGCCGGCGTAGGGGCCGGTCAAGGGGCCGGTCA
 TCGGTTCCGCCGCTCATGAGATCCGCCAGCACGGCACGCCGGTGCAGGCCAGCAGCCGTTGCGGTAGTGGCCG
 GTATTCAGCCAGGCCGCTGCAAGCCAGGCCGATATAGGGATGCTTCGGGAGAGCCGGCAACCCCTGC
 CCAGTGGCCACCGGCTGCATGTCGCGCAGTCCGGCAACAGTTCTGCGCAGACGCCCTGAGGCTTCCAGCGCTCG
 CGGTGGCGTCTGCGAAGCCGAATGTTCAAGGTGCTGCCATCAGGATGTGGCGTGCAGGCCGGAAATCGCGTAG
 CGCCCTTGGCCAGCACCATGCGGGCAGGAATCCGCCGCACTTGTAGAGGATCATGACCTTCAACCGGTACCC
 GGGCAGTCCAGGCCAGCGCTCAACAACTCGCCGCTCAGGCCCTGCCGCCAGCAGCACCTGTCGCCACGGATCT
 CGCCACGCCAGGTGCCACGCCACACTCGATGCCGTCGCGCAACCAGCCGCCACCTCCGCTGTTCATGCAACTCG
 AGATTGGCAATTGTTGCAAGGATGCCGCAATGA

>ORF33705c (SEQ ID NO:366)

GTGATATTCTCTGTCCTGGCAATCGGTAGGAGCCCTGTTGAGTAGAGATGTTAGTGTAGTGGTAGGCCTGGCGTCAT
 CGGCTGTTGACGCCGGAGCTGGCCTGCCGGACTGGGGTACCCCTGGTGGAGCGGGCGAGAGTGGCGTGAGG
 CATCCCTGGCGGGAGCGGGATCGTCTGCCGCTATCCGCGCTACAGCCCGGGTGCACGCCCTGGCGACTGG
 TCGCAGGACTCTACCGGCCCTGGGCAGCGTTGCTCGACGAGACCGGGCTGATCCGAGGTCCATACCGTTGGCCT
 GTACTGGCTGGACCTGGACGACCGAGCCGAGGCCTGCACTGAGTGGCAGCACCACCCGGCGTTGAAGGAAGTGC
 TCGAGGAGGCTACGCCGGTGGCGCAGGCTTCCAGCGGGCGTCTACATGTCGGCGTGGCCAATGT
 CGCAATCCTCGCCTGGCGCTCATTGCGGCATCCCTGCAACAATTGCGCAATCTCGAGTGTGCATGAACAGACGGAGGT
 GCGCGGCTGGTTGCGCGACGGCGATCGAGTGGTGGCGACCTCGCGTGGCGAGATCCGTGGCGACAAGGTGTC
 TGGCGCAGGCCCTGGAGCGGGAGTTGTAAGCGCTTGGCTGGAACCTGCCGTGGTACCGGTAAAGGTCA
 ATCCCTACAAGTGCAGGCCGGATTCCTGCCGCGATGGTGTGGCCAAGGGCGCTACCGGATTCGCCGGCAGCG
 CCACATCCTGATCGGCAGCACCTGGAACATTGCGCTTCGACAAGACGCCGACCGAGGGCGTGGAAAGCCTCAGGG
 CGTCTGCCGAGAACTGTTGCCGAACTGGGGACATGCAAGCCGGTGGCCACTGGGAGGGTGGCGCCGGCTCTCC
 GAAGGCATCCCCATATCGGTCCGGTGCCTGGCTTCGACGGGCTCTGGCTGAATACCGGGCACTACCGCAACGGGCTGG
 CCTGGCACCGCGTGTGCGCTGCTGGCGATCTCATGAGCGGGGGAAACCGATCATGACCCGGCCCCCTACGCC
 CGGCTGGCGCTCTGA

Fig. 3-31

>ORF32832 (SEQ ID NO:368)
GGCTTCAGCGCTCGTGGTGGCGCTTGTCAAGGCCGAATGTTCAAGGTGCTGCCATCAGGATGTGGCCGTGCGCCGGAATCGCGTAGCGCCCCCTGGCCAGCACCATGCGCGCAGGAAATCCGCCGCGCACTTGTAGAGGATCATCTGACCTTTACCGGTACACGGCAGTCCAGGCCAGCGCTTCAACAACTCGCCGCTCCAGGCCGCTGCCGCCAGCAGCACTTGTGCCACGGATCTGCCACCGCACGGTGCACGCCACTCGATGCCGTCGCCAACAGCCGCGCACCTCCGTCTGTTATGCAACTCGAGATTGGCAATTGTTGCAAGGGATGCCGCAATGAGCGGCCAGGCAGGATTGCGCACATTGGCCACGCCGACATGTAGACCGCCCGCTGGAAAGCCTGCCAGGCCGGCACGCCGCGTAGGCCCTCTGATGCCACCTTCCCTCAACGGCCGGGTGTGGTGCCTGCCACTCGCAGTGCCTCGGTCTGGTCGCCAGGTCAGGCCAGTACAGGCCAACGGTATGGACCTCGGGATCGAGGCCGGTCTCGTCGAGCAAACGCTGCCAGGGCCGGTAGAAGTCTGCGACCACTCGCCAGGGCGGTACCGCCGGGCTGTAGGCCACGGATAGAGCGGGAGACGATCCGCCCTCCGCCAGGATGCCCTCACGCCACTCTGCCCGCTGCCACAGGGTCAAGGTCAAGGCCAGTCCCGGGCGGTCAACAGGCCAGTGA

>ORF33547c (SEQ ID NO:370)
GGCATCTGGCGGGAGCGGGATCGTCTGCCGCTATCCGTGGCGTACAGCCCGGGTACCGCCCTGGCGCACT
GGTGCAGGACTTCTACCCGGCCCTGGGGCAGCGTTGCTCGACGAGACCGGGCTGATCCGAGGTCCATACCGTTGGC
CTGTACTGGCTGGACTGGACGACCAAGACCGAGGCAGTGGCACGCCAACACACCCGGCCGTGAAGGAAGTGC
GATCGAGGAGGCCTACGGGGCGGTGCCCGGCTGGCGCAGGCTTCAGCGGGCGGTACATGTCGGCGTGGCCAATG
TGCAGAACATTCCTCGCTGGCGCGTCAATTGCGGGCATCCCTGCAACATTGCGCAATCTCGAGTTGCATGA

>ORF33205 (SEQ ID NO:372)
GCGGCCAGGCAGGATTGCGCACATTGGCACGCCGACATGTAGACCGCCGCTGGAGGCCTGCGCCAGGCCGGCA
CCGCCGCGTAGGCCTCTCGATGGCACTTCCTCAACGGCCGGGTGTGGTTGCGTGCCTACTGCAGTGCTCGGTCTGG
TCGTCCAGGTCCAGCAGTACAGGCCAACGGTATGGACTCGGGATCGAGCCGGTCTCGTCGAGCAAACGCTGCCCAAG
GGCCGGGTAGAAGTCTCGCAGCCAGTGCAGGCCAGGGCGGTACCGCCGGCTGTAGCGCCACGGATAGAGCGCGAGACGA
TCCCGCCTCCGCCAGGATGCCTCACGCCACTCTCGCCCGCTCACCAGGGTACCCGCACTCCGGCGAGCGCCAGC
TCCCGGGCGGTCAACAGGCCAGTGCAGGCCAGGCCTACCACTACATCTACTCACCAAGGGCTCTACCGATTG
CCAGGAACAGAGAAATATCACTCAAAGGGATCAGATGCTGACGAATTGCCTGCTCAACGAACCTAGTCGAATCTAGTCC
CGGTGAAAAGGCCATCATACCCGAGGGTATTCACTCCATGA

>ORF33512 (SEQ ID NO:374)
AGCGGCAGACGATCCGCCCTCCGCCAGGATGCCTCACGCCACTCTGCCGCTCCACCAGGGTCACCGCAGTCC
GGCGAGGCCAGCTCCGGCGTCAACAGGCCAGTGCAGCCAGGCCCTACCACTACTACATCTACTCACCACAGGGC
TCCTACCGATTGCCAGGAACAGAGAAATATCACTCAAAGGGATCAAGATGCTGACGAATTGCCCTGCTTCAACGAACTCAG
TCGAATCTAGTCCCAGTAAAAGCCCATACCCGAGGGTATTCACTCCCATGAAATCGAGTGGTTGAATTGGTGG
AACTATCGATAGTCCTATCGATCCTTGCAGAGCGTACAATTGCCTGCCACCCCTCCCCGACAGAATGAAGCGGGAC
ATTAG

>ORF33771 (SEQ ID NO:376)
AAAGCCCATCACCCGAGGGTATTCATCCCATGAAATCGAGTGGTTGAATTGGTGGAACTATCGATAGTCCTATC
GATCCTTGCATAGGCCTGACAATTGCGCTGCCACCCCTCCCCGACAGAATGAAGCGGGACATTAGCCGTGATATTGGTG
ACAGCCTGACTAGTCATGTGATGGCTGCGCGGGCTAGCAGCATACAGAACGGCGTGTACAGGAGTGTGCGGTAGCGGT
GACGGCAGTACCTGCAGCGAGGAATGGCATCTGGCTGGTTCAAGCCGTAAAGCAGGAGCCAACAGATACTGGCCCGCA
TGAAAATACGAGTCGCACCGATATTCAATTGGCGGGGCTTCGACAAGCGACTGCGCTACCTGCCTAATGGCACCAGCCCTA
CAGGTAACGGCGTTCTTCGAATGTAAGGACGATCGCATCGAGTGGCAATTGGTGTCAATCGGCAAGGCCGCTCAGG
GTGGCGGGAAAGAGCGAAAATAAAGCTCTTACCTGTGCTCCAGGCGGTGA

>ORF34385c (SEQ ID NO:378)
TGGAGAGCGCATTGCTCTGTAGCAGAGACAGCCGGAGCGGAGAGTGGGATGACTGGCAAACGGTATGTGAAACAGTTCT
CTCACCGCCTGGAGCACAGGTAAAGAGAGCTTTTATTTCGCTTTCCCGCACCCCTGAGGGGGCTTGCCATTGAGC
ACCAATTGCCACTCGATGCGATCGTCTTACATTGAAAGAAACGCCGTTACCTGTAGGGCTGGTGCCATTAGGCAGGTA
GCGCAGTCGCTTGTGCAAGCCCCGCAATGAATATCGGTGCGACTCGTATTTCATGCCGGGCCAGTATCTGTTGGCTCC
TGTGCTTACGGCTGAACCAGCCGAGATGCCATTCTCGCTGCAGGTACTGCCGTACCGCTACCGCACACCTCGATGATC
ACGCCGTTCTGTATGCTGCTAGCCCGCGCAGCCATCACATGACTAGTCAGGCTGTCACCAATATCACGGCTAATGTTCCG
CTTCATTCTGTGGGGAGGGTGGGCAGCGCAATTGTCACGCCATACGCAAGGATCGATAG

Fig. 3-32

>ORF33988 (SEQ ID NO:380)

TCATCGAGGTGTGGTAGCGGTGACGGCAGTACCTGCAGCGAGGAATGGCATCTCGGCTGGTCAGCCGTAACGACAGG
 AGCCAACAGATACTGGCCCGGATGAAAATACGAGTCGACCGATATTCAATTGGCGGGCTTCGACAAGCGACTGCGCTA
 CCTGCCTAATGGCACCGCCCTACAGGTAACGGCGTTCTCGAATGTAAGGACATCGCATCGAGTGGCAATTGGTGC
 TCAATCGGAAGGCCGCTCAGGGTGGCGGGAAAGAGCGAAAATAAAAGCTCTTACCTGTGCTCCAGGCAGGTGAGAG
 AACTGTTTACATACCGTTGCCAGTCATCCACTCTCGCTCCGGCTGTCTGCTACAGGGACAATGCCTCTCCACT
 AG

>ORF34274 (SEQ ID NO:382)

AAAGCTCTTACCTGTGCTCCAGGCCGTGAGAGAACTGTTCACATACCGTTGCCAGTCATCCACTCTCCGCTCCGG
 CTGTCTCTGCTACAGGGACAATGCGCTCTCCACTAGGCAAGATTATCTGGCCCTTTCCCTGTTGGAGTACTGCATGCGCT
 CTATTTGTCGAGCGCCGGCTTTCCCTGATCGAGGCGAACCGAATCCAGACTGCGCAGCGAGGAACACTACAGCCTGCTTCAGTACGC
 TCGCAGCGAAGCTGTAACCGTCATGCCATGTGAGCATAGGGCAGCGAGAACATGACTGGCAAAGGCCCTGGAAA
 TCATCAGCGGCGCGACCACCGTGCAGGAAAGCAGCAACAGGTTCCAGCAGGTCTCGCTATCCGCCAGCAGTGCAGTGCAG
 CTGACCTCAACGCTACCGGCACACTTAGCAACAGGCTGCAAACATTGACATAAAGGTCTGCTCGCCGGTGCAGAAAAG
 TACAGGACGTCTGCTTACCGTTAGGCCAGTGGACGCGTGTACCCATCTCAAGCAACCGGACAGCTGTA
 ACT
 GA

>ORF34726c (SEQ ID NO:384)

CGAGACCTGCTGGAAACCTTGGTGCCTTGCACGGTGGTCGCGCCGCTGATGATTCCAGGCCTTTGCCAGTCATTGT
 TCTGCGTCCCTGATGCTCACATTGGCATGACGGTTACAGCTCGTGCAGCGTACTGAAGCAGGCTGTAGAGTCC
 TCGCTGGCAGTCTGGATTGGTGCCTCGATCAAGGGTTGAAACTGGTACGCAATGCTGGCAATATGGCAGCAG
 AACCAACACCATCATCAACTCGATCAGGGAAAGCCGGCCTGCGACAAATAGAGCGCATGCACTTCCACAAGGAAA
 GGGCCAGATAATCTGCTAGTGGAGAGCGCATTGCTCTGAGAGACAGCCGGAGCGAGTGGATGACTGGCA
 AACGGTATGTGAAACAGTTCTCACCGCTGGAGCACAGGTAA

>ORF34916 (SEQ ID NO:386)

GGAAAGCCATGTCTCGAGAAACGGGTTTCAGCATGATCGAAGTACTGGTTGCTGGTGTGATCAGCATTGGCTACT
 GGGCATGGTGCCTGCAAGGGCGCAGATCCAGTACACCGAGGTCGGTACAACGCAATGCCAGCAATGCTTCTA
 GCGACCTGATGGAATAATGCGTGCACCGAGATGCCGTACTCAATCTACGCCCAACTACGCAAGACTCGTCTAC
 TACAAGGCAAGGGCAGCGACTTCCCGCAGCCCCAGCGCGTGCACCGCATTGCCAGATGCTAAGGAACGTCTCG
 CTGCTGGGCCAACAGGCTCGAAAGACTTGGCGGGAGCCTCCGACTCTGAATAGCCAATTCTACATTGTCGAGCC
 CAACCCGGGTACCTGCGACAACACCAAGGCTGCCATCGAAATCCAGGTTGCCAGGCTGGCAGCCATGGATGGAGCGTGT
 TTCAACGCCCTGACTCCACCTGTGCACTACAGCGTCCGCTCCGAATTGTGA

>ORF35464c (SEQ ID NO:388)

AGAGCATGCTTGTCTACAATTGGAGCGCTGTAGGTGCACAAGGTGGAGTCAGAGGCGTTGAAACACGCTCCAT
 CCATGGCTGCCAGGCAACCTGGATTTCGATGGCGAGCCTTGGTGTGCGAGGTACCGGGGTTGGCTGCGACAA
 ATGAGAATTGGCTATTCAAGAGTGCAGGGCTCCCGCAAGTCTTCGAGGCTGTTGGGCCAGCAGCCGAGACGTT
 CTTAGCATCTGCTGGCAATGGCGCGAGCGCCTGGGCTGCGGGAAAGTCGCTGCCCTGGCTGTAGTAGACCGAGT
 CTTCGCGTAG

>ORF35289 (SEQ ID NO:390)

ATAGCCAATTCTACATTGTGCGGCCAACCCGGTACCTGCGACAACACCAAAGGCTGCCATCGAAATCCAGGTT
 GCCTGGCGAGCCATGGATGGAGCGTGTTCAGCAACGCTGACTCCACCTGTGCACTACAGCGTCCGCTCCGAATTGTG
 AGAACAGCATGCTCTCAGCAAATGCAAGAAAGGCTATCGATGGTAGAAGTGCCTGTTGGCAGTCGCTATAAGCAGCTT
 CCTGATCCTGGGATGCCAGATCTACATCGACAACACGCAACTATCTTCCAGCAAGGCCAGGCCGGCAACCAGG
 AAAATAG

Fig. 3-33

>ORF35410 (SEQ ID NO:392)

CTCCACCTTGTGCACCTACAGCGTCCGCTCGAATTGTGAGAACAGCATGCTTCAGCAAAATGCAGAAAGGCCTATC
 GATGGTAGAACGTGCTGGCACTCGTATAAGCAGCTTCTGATCTGGGATCAGCCAGATCTACATGACAACAAAC
 GCAACTATCTTCCAGCAAGGCCAGGCCGAACCAGAAAATAGCCGTTCTTATGCTGCTGCAGCAACAAC
 GATAAGACAGCCTATCGTCGCTTCACGACGACAACATGGAGAATGCTTCAAATCCGCACATTCAATGGCTGCGTGC
 ATTGTGGCTGGCGAGACTATCGTCGCGCACTGCCCTCAAGGGGTGAGTACGGTGTCTGCTTGCCTATCAACCC
 CCTACAAAGGGAGCATGATTGCTCGTAATGAAATTACCGGAGTCCGAAAGGCCCTCAAAATACTCCCCCTGTC
 GTCGTTGCCCTGGCTACCTACGAGCGCCGGTACCCGTAGTTGAGTCAGTCGCTCCGATATGCCAGTCGAATCGGAGA
 ATTGGTCAGTGGCTCACAGACTCCGCTTGGAGCGGGGGTGGCAGCAGATCGTAGCGAACGCAAAGTATCCAGCT
 TCGTCGCACTACAGGATGTGCCGGTGTCTTATCCGAGATTGCGCTCTCAATCCTGGCAGCGAGCAGAACATACAAGC
 CTGCGCACAGGAGATGATAGCCAGGCACGCGATCGTGGATCGCTTATCCGAGAGCAGAACAGGCCATCGAGGCCGC
 AGACAAAGGCCAGATTACCAAATAGCGCTGGTAACCAAACCATCAGGAATCTCATGCCATGA

>ORF35907c (SEQ ID NO:394)

GTAGACCAGGCGAACGACGACAGGGGGAGTATTGTGAAGGGCTTCCGAACTCCGTAATTTCATTACCGAGGCAAT
 CATGCTCCCTTTGTAGGCGGGTTGATGCGAACAGCACCGTACTCACCGCCTGAGGGCAGTTGCCAGCGATA
 GTCTGCCAGCCACAAATGCCACGCCATTGAATGTCGGATTGAAAGCATTCTCCATGTTGTCGTCGTGAAGGG
 ACGATAGGGTGTCTTATCCAGTTGCTGAGCAGCATAAGAACGAGCGCTATTTCCTGTTGCCGGCTGGCCTT
 GCTGGAAAAGATAGTTCGTTTGTGTCATGATGAGTCGCTGATCCCCAGGATCAGGAAGCTGTTATAGCGAGTGCC
 ACGAGCAGTTCTACCATCGATAG

>ORF35534 (SEQ ID NO:396)

TCCTGGGGATGCCAGATCTACATCGACAACAAACGCAACTATCTTCCAGCAAGGCCAGGCCGGCAACCAGGAAAAT
 AGCCGCTTCGTTCTTATGCTGCTGAGCAACAACTGGATAAGACAGCCTATGTCGCCCTCACGACGACAACATGGAGAA
 TGCTTCAATCCGCACATTCAATGGCTGCTGCATTGTTGGCTGGCAGACTATGCTGGCAACTGCCCTCAAGG
 CGGGTGAGTACGGTGTCTGCTGCTATCACCCGCTACAAAGGGAGCATGATTGCTCGTAATGAAATTACCGGA
 GTTCCGGAAAAGCCCTCACAAATACTCCCCGTGCTCGTCCGCTGGTACCTACCGAGCGCCGGTACCCGTGA

>ORF35930 (SEQ ID NO:398)

GTTGCAGTCGTCCCAGATCGCCCAGTCGAAATCGGGAGAATTGGTCAGTGGTCTCACAGACTCCGTTGGAAGCGGGG
 GTCGGGCCAGCAGATCGTAGCGAACGAAAGTATCCAGCTCGCAGTACAGGATGTCGCCGTGCTTATCCGAGC
 ATTGCGCTCTCAATCTGGCAGGGCAGCGACAATACAAGCCTGCGCACAGGAGATGATGCCAGGCACGCGATCGCTGGA
 TCGTCCTTATCCGAGAGCAGAACAGGCCATCGAGGCCAGACAAAGGCCAGATTACCAAATAG

>ORF36246 (SEQ ID NO:400)

CCAAACCATCAGGAATCTCATGCCATGACCTGCCATACCTCTGACAGCAGGGATCCACGTTGTTGATCTGCTGGT
 TATCTTGTGATGATCACGCTCTGCCGTTCCAATGCGCAGGTGCACTGAAAGCCGTATCACGCCAATCTCA
 TCGAACAGAACGCCCTGCCAATGCCGGCGAAGCTGGCTACGCGAAGGTGAAAGCAGCTTTCATACCATCAAGCCC
 CCAGAGGTGGCAGCGATGCCGATAGCAATGTCACCGGCTTGCAACTGAACTGAGTGCCTCTCCGTACCCCG
 AGATGACGTGACAACAAATCCGGTGGCAGCCCTGAAACGGCAAGACAGATAACGCCAATTACGTTCTGGATGCCCTACC
 GAGGCAGCGATCTGAATAACCCCTACGCGATCGACAAAGACCGCGCAGTCACCTGGCAGACCATCACGGTGCCGCTGGC
 GAACAGAACACGAAGCGAAAATCCGAGTACGGCAACATGATGCGGGGTCGGCAGCTACTACGAAACCAACAG
 CGCGCCCTCAACAAGCGGGCGGAGAGACTGTTCTACAGGCCGTTCATGCACGCCGTATACCAAATG

>ORF26640c (SEQ ID NO:402)

GGCATCCAGACACGTGAATTGGCTTATCTGCTTGCCTCAGGGCTGCCACGGATTGTTGTCACGTATCTCGGGG
 TACGGAGAGGGCACTCAGGTTGAGTATGCAAGGCCGTTGACATTGCTATCGGCCATCCGCTGCCACCTCTGGGGCT
 TGATGGTATTGAAAAGCGTCGTTACCTCGCGTAGCCCAGCTCGCCGCTTGTGCGAGGGCCTGTTGATGAGA
 TTGCCGGTATGACGGCTTCCAGTGCACACCTCGCGCATGTTGGAAACGGCGAGGAGCGTGTATCAACAGATAACCAG
 CGAGATCAACACGTGGATCCCTGCTGCGAGAGGTATGCCAGGGTATGGCATGA

>ORF36769 (SEQ ID NO:404)

TGCGCGGGGTCGGCACGTTCTACTACGAAACCAACAGCCGCGCCCTAACAAAGGCGGGCGGAGAGACTGTTCTACAGGCC
GTTCATGACGCCCTGTTACCAACTGACTGGAGGCCAGGCATGATCACCAGATTACCCGCCAGGAAAAAGCCTGCTGG
CTGCAGGGTGCACCCCTGAGCATCTGTCGCCCTGACAGTTATGCCGCCAGGCCCTGAATGTCAGCCAGCAACCCCTG
TTCCATAACCCAGGGCGTTGCTCCAAACCTGCTGTTCACTCTAGATGACTCAGGCAGTATGGCCTGGCTTACGTGCCCGA
CGGTATTAGCGGAAATAGCGGAGAGCGGGAGCTCCAGCGATTACAAACGCACTGTTACTACAAACCCGATTATGCTTAC
AAGTGCCAAGAAATTGACACTGTCAGGCATCAGATCATGTTCCGACTATCCAGTGCCACGCCCTCACAGCAGCCTGG
CAGGATGGCTACGCCAAGGCTCACCACCAACCTGAGCAATAACTATGCCCTCAATGGGAACCGGCTGGCTGGTTG
CATCGATAGCAGCTGCAATACCGGGAGAGCTTATTACTATCTAAAGGTAAAGCGTAGCTGCCCTGACAGCCGGTGA
GCAGCTCCAACCTCTGTTATACCTACAATGCTCTTCTACCAGTCAGGAAAGCAACTTGGCATATGGTACTCTACTAT
CGCAACCGCATTCTGCCACAAAGACCGCTGCCAACCTGGCTTTACAGCCTGCCGGAAACGTGCGTCTACTTGGGG
GGCCCTGAACACCTGAGCATGGCGCAAACAGCAGAACGCTGCCAAAACAATGCCCTGCTCCAATTCAACAAGCAGCACA
AAATCAATTCTTCATTGGCTGGCGAACAGCCGGCAGCGCGGGTACTCCTCTGCTGCGGCTTGTGACCGAGCCGG
CGCTTCTGCAAACCAACGGCACAGCTTATACCACCGAAGACGGAAGACATATTCTGCCGGGCCAGCTATCACATCAT
GATGACCGACGGTACTGGAACGGTCGGAACGTCACCCCCGGCAATCTGACAACAGAACAGACCTTCTGATAGCA
CCCTCTATAGGCCACAGCCCCCTTATGCCGACAGCAATGCCAGCTCATTGGCTGACCTGGCTTCAAATACTGGACCAACA
GACTTACGTCCCAGCATGACAATGACCTGAAGCCTTATGCCCTACAAGAGTGGGGACGATTCCAAGGATTACTGGGA
CCCTCGCAACAACCCAGCCACTTGGCAACACATGGTCAACTTACCGTGGCTTAGGTCTTCTATTGCTCACATTGA
ACTCTGACCAACTTGGACAGGCAGCACTTGGCAACTACGAGGAGTTGATGGCTGGAAGCAAGGCTTGGCCAGCGTC
GATAACGACGCCGACCCGGTAACGCTACGACCTCTGGCATGAGCTATCAACTCTGCTGGAGACTTCTTAGCGCGGA
ATCACCGGACTCTGGTTCAGGCTTCAATAAGATCTGACACGGATTCCGAGCGCAACACCTCTCTCCAAACCAAG
CAATGACTTCCGCGCTGCAAGGATGACGGAACCGCGACAAGCTGATCCGCTACAGCTACCGTCCAGCTTGGCCAGTGAC
AAGAACTGGCGGGCGACCTTATACGTTACAAGGTGGAGTCGACTTCCACGGGTCGACCAAACCCAGGAATGGAGCGC
CGGCGCACTGCTGGACAACCGAGCTCCCGCTACCCGTAATATTACATGCCAGCAATAGCGGAACCAACCGCTTAAGC
CTTTCACATGGAGCAATATTGGGGAGTCAGTTAGCCACTTGGCTGAAACCGCAACCCGGACAAGGACAATCAGGCCGAC
ACCAAAGGAGCACAGCGGTCGACTTCATCCGTTGGCCAGCAGAATATGGATGGATTCCGGCAACGACAGCGGTTAGG
GGACATCGTCACTGCTCCAGCCGTGGTGGACCGGGCCAATACCTCACTTATCTGGCCAACCCATCGAACCCAGCG
GCGACTACGGCACATTCAAGACAGAGGCAGACCGCAGCCCTAGAGTTATGTTGGATCCAACGATGGCATGTTGCT
GGTTCAACATCAAACCGCGTGGAAAGAGTTCGTTTACAGCTTACAGCTTACCCCTACAGCAGTATTGAAAGCTTAACAGCTTACCGG
CATCAGCTTACCGGGCGGTGCCACCAATATTGCTGCACTGCTACACCCGGTGTGAGCTGCTTACCGGCTTTCGATGGAGCTT
GGCACACTGTTCTGATCGGAACGCTTGGTGTGGAGGTGCGGGCTGTTGCACTGATGTAACCAAGCCGGACGATGTC
AAGCTGTTGGAAATCGATAGCAGTACCGACTCGGACCTTGGTACACCTTCTCCAAACCTACCGTAGGCCAGACTGCA
CAGCGACAATGGGAGTCAGTTACCGCAACGGCTATGGAAGCGATAATGACAAGGAGCTTACTGCTGATTGATTGA
AAAAGGAAACGCTGATCAAGAAGCTGGAAAGTCCAAGCGAGCGCGAATAGCAATGGCCTATGACGCCCTCGCCTGGCT
GATAACAAACAGCGATGGCATTGCTGACTACGCCATTGTCAGGAAATATCTGGCGCTTGCAGGGAAATATCTGGCGTTGATTTGATCGG
CAATACCGCAACGACGACCCAGACACAAATACCTCATCAATCCCTCAAGCCGGAGATGTAAGATCTTCTGCTTCA
GAGTATCGTTAGCGCGCCCGCTTTCCGTGCTCGCGCCAGACAACAATACTCGTACGCCATCACGGCTCCGCCCTAC
TTGGTACGCCATCTAGCGTAAGGGCTACATGTCATGTTAGGACAGGAAATACTTCGAGGACGATGACGCTCAGGC
CGATACCGCCAGGCCATGACGCTCTATGGTATCTGGATGCCAGACCAAGGGCGAAAGCGAAACAGTACCCAAACCA
TCGACCGCAACGCCCTCACAGCCAAACCATGACAACAGAGGCAGCTCCACATTGGTAGCGTGAACAGGAATATTGCG
CTTATTAGCCAACCCGGTGAAGTGGTACAAGAGCAGGAGCAACCCGGTACCGCGAACTCGGATGTTGCTAGCTATGCTG
GCGACTGAATCTGGAGGTCAATAGCAGCAAGAAAGGCAAATGATGATGCAAGGATATGTTGCTGCGCCAGTGGCTTC
TATTGCAAGACCTTGACACCGAACGACGACCCCTGTGACAGCGGCTTACCGAGCTGGACCTACGGCCTCAATCCATATACT
GGCGGACGTACCACTGTTACCGCTTCTGATCTCAAACCGTGGGGTATAGTGGACTCTGGCTGGATTACAACGGCTCGGT
CGTATCCGCCCTTCCAACAGGATGGACTAGGTGGCTGGCATTACCGAGAACGCGTCAATCGAGGCTTGCAGT
GTGATGAGTGCATCATCTTCAACCCAGCGACAAGAGTAACGGACGACAAACCTGGGGTCTGCGAGGAGAAATGA

Fig. 3-35

>ORF37932c (SEQ ID NO:406)

GCTGGCATTGCTGTCGGCATAAGGGGGCTGTGGCCTATAGAGGGTCTATCAGGAAAGGTCTGGTCTGGTGTGAGAT
 TGCCGGGGGTGACGTTCCGACCGTCCAGATACCGTGTGTCATCATGATGTGATAGCTGGCCCGCAGGAATATGTCTT
 CCGTCTCGGTGGTATAAGCTGTGCCGTGGTTGCAAGAAGCGTCGGCTCGGTCAGAGGCCATGCAGAGGAGTACC
 GCGCTGGCCGGCTGTCGCCAGCCAAATTGAAGAAATTGATTTGTGCTGCTTGTGAATTGAGCAGGGCATTGTT
 GGCAGCTCTGCTGTTGGCGCGATGCTACAGGTGTTCAAGGGCCCCCAAGTGAGACGCACGTTCCGGCAGGCTGAA
 AAGGCCAGGTTGGCAGCGTCTTGCCAGGATGCGGTTGCGATAGTAGGAGTACCATATCGCAAAGTTGCTTCC
 ACTGGTAGGAAGAGCATTGAGGTATAACAGGAGTTGGAGCTGCTACCGGCTGTGCAAGGGCAGCTAGCGCTTACCTTAT
 AAGTATAGTAAATAAGCTCTCCGGTATTGCAAGCTGCTATCGATGCAACCAAGCCAGCCGGTCCCCATTGAGGGCAGTAG
 TTATTGCTCAGGTTGGTGGAGCCTTGGGGTAGCCATCTGCCAGGCTGTGAAAGCGTGGCACTGGATAGTCGGAA
 AACGATGATCTGATGCCGTGA

>ORF38640c (SEQ ID NO:408)

CTGACTTCCTCAATATTGCTCCATGTGAAAGGCTTAAGCGGTTGGTCCGCTATTGCTGGCAGTGAAATATTACGGG
 TAGCGGGAGCTCGGTTGTCAGCAGTGCAGCCGGCTCATTCCCTGGGTTTGGTCGAACCGGTGGAAGTCGACTCCACC
 TTGTAACGTATAAGTCGCCGCCAGTTCTGCACTGGCAAAGCTGGACTGGTAGCTGTAGCGGATCAGCTTGTGCC
 GGTCCGTACCTGCAAGCGCGGAAGTCATTGCTGGTTGGAGGAGGTGTTGCCCTGGAAATCCGTGTCAGGATCT
 TATTGAAAGCCTGAACCAGAGAGTCCGGTGA

>ORF39309c (SEQ ID NO:410)

AGCTGCCTGTCAATTACGCTTCCATAGCCGTGCCGTAACTACTGCCCATGTCGGCTGTCAGTCTGGCTACGGTAG
 GTTTGGAGAAGGTGTAACCAAGGTCCGAGTCGGTACTGCTATCGTATTCCCAAAGCAGCTTGACATCGTCCGGCTTGGTT
 ACATCGAGTGCAGACAGGCCGCGACCTCCAGCACCAAGCGTCCGATCAGAACAGTGTGCCAGCTCCATCGAAAAAGGC
 ATCGCTGACGACCGGTGAGCGTCAGCAAAATTGGTGGGACCGCCCTGGTAGCTGATGCCGTAAGCTTGTAAAGCT
 TTTCGAATACTGCTGTAGGGATGAAAGCAACTCTCCACGCCGGTTTGTGTTGAAACCATGCAACATGCCATCGTG
 GATCCAACATAAAACTCTAGGGCTGCGCTGGCTGCCTGTCTGAATGTGCCGTAGTCGCCCTGGGTCATGGGTT
 GGCCAGATAAGTGAGGTATTGGCCGGTCCGACCACGGCTGGAGACGAGTCACGATGTCCCCCTAA

>ORF38768 (SEQ ID NO:412)

GGGACATCGTCACTCGTCTCCAGCCGTGGTCGGACCGGCCAATACCTCACTTATCTGCCAACCCATCGAACCCAGC
 GGCAGACTACGGCACATCAAGACAGAGGCCAGACGCCCTAGAGTTATGTTGGATCCAACGATGGCATGTTGCA
 TGGTTTCAACATCAAACCGGCGTGGAGAGGTTGCTTCCATCCCTACAGCAGTATTGCAAAGCTTAACAAGCTTACCG
 GCATCAGCTACCAAGGGCGGTGCCACCAATTTCGTCAGCAGTACCCGGTGTAGCGATGCCCTGGGTCATGGGTT
 TGGCACACTGTTCTGA

>ORF40047c (SEQ ID NO:414)

AAGCACTGGCCGGCAGCGAACATATCTCGATCATTCGCTTCTGCTGCTATTGACCTCCAGATTCACTCGCC
 AGCCATAGCTAGCCACATCCGAGTTGCGCGTACCGGTTGCTCCGTTGCTACCACTTCACCGGGTTTGGCTAATAAGC
 CGAAATATTCTGTTCACGCTACCGAATGTGGAGTTCGCTCGCTGCTGGTACCGGTTGCTGCTGCTGGCTGCTGCTGAT
 GGTGGGGTACTGTTGCGTTCCGCCCTGGTCTGGCGATCCAGATACCATAGAGCGTCATGGCTCGGTGGTATCGG
 CCTGAGCGTCATCGTCCCTCGAAGTATTTCCTGTAACCTACGATGACGATGTCAGCCCTAACGGCTAGGATGGCGTACCAAG
 GTAGGGCGAGCGTGATGGGCTGACGAGTATTGTTGTCGGCGCGAGCACGGAAAAGCGGGGCGCCGCTGAAACGATACTCT
 GAAAGCAGAAGGATCTACATCTCCGGCTGAAGGGATTGATAGAGGTATTGTTGCTGGGTCGTCGTGCGGGTATTGCA
 CGATCAAATCGAAGGCCAGATATTCCCTGCACTGCCAGCATAGCGTAGTCAGCAATGCCATCGTGTGTTATCA
 GCCAGCGAGCGTGTGATAG

>ORF40560c (SEQ ID NO:416)

CCGGCGAGTCCTGTTGGACACGGTTGGCAAGCGATATGTCGCCCCATCGACTACTACCAAGACCGGCCAGGATGA
 ACATCCCTGACCACGCCACATTCTCGAACGTATTGTCGGCACTCAAGCAAAGGTTGGCAAGCCAGAGCTAGAGCTGC
 AAGAGCTGTCGGCAGAACGCTAAGGGTTCATGTTATTCTCCCTGACGACCCGCCAGGTTGTCGTCGTTACTCTT
 GTCGCTGGGGTGAAGATGATGCACTCATACCGAGTCAGCAGCTGGATTGACGCTGTTGTCGTTCTGGGTAATGGCCAAGC
 CACCTAG

>ORF40238 (SEQ ID NO:418)

GTGGCTTGGCCATTACCCAGAACAGCGTCAATCCGAGGCTGACTGGTATGAGTCATCATCTCAACCCAGC
 GACAAGAGTAACGGACGACAAACCTGGCGGGTCTGCGAGGAGAAATGAACATGAACCCCTAACGTCTCGCCACAGCT
 CTTGCAGCTCTAGCTCTGGCTTGCACCTTGAGTGCCAGAACATGAGAATGTGGCGTGGTCAGGA
 TGTTCATCCTGCCGCCGGTCTGGTAGTAGTCGATGGCAGACATATCGCTTGCACCAACCGTGTCAACAAACAGGACTCGC
 CGGTACATATTCTGGTACGTACGGACAGACAGTGTCTTCTCCGGAAACTCACCAGCAGCTGCCAGAAATCGAGTC
 TTCTACATTATCAAGCAGGCCCTCTGTTCCCTCGGATCGGAGCAGCAACAATGAAGTCGAACAGAGGGCTTCACTCTC
 ATCGAGTTGATGATCGTAGTAAATCATCGTATTCTGCTGGTATCGCTAACCCAGCTACGACGAATACGTGAAGCG
 CGGAAATCGCACCGAAGGGACAGGCATTACTCAGCGAAGCAGCCGCTACTCAAGAGCGTATTTTCACAGAACAAACTT
 ATATCACTACCCAAGCGACATCGCAAGCTGCATATGCCAACACATCGGGCACACAGTGAAGTCCTCACAGGAAA
 TACAGCCTACCGTCGATACGGTAGCCAACGAGGAGTTATCGCTTACCGGATTCAACGATCTGATG
 TGGCAACCTGACCTGACCGCAACGGCGAGAAAGGCCGACTGGAAGCAAGAAGAGCGTTGCAAGATGCTGGCGCTAA

>ORF40329 (SEQ ID NO:420)

CGGACGACAAACCTGGCGGGTCTGAGGGAGAAATGAACATGAACCCCTACGTCTCTGCCACAGCTTGCAGCTCT
 AGCTCTGGCTTGCACCTTGAGTGCCACGAATACGTTGAGAATGTGGCGTGGTCAGGATGTTCATCCTG
 CCGCCGGTCTGGTAGTAGTCGATGGCAGACATATCGCTTGCACCAACCGTGTCAACAAACAGGACTGCCGGTCAATATTC
 TTGGTAGCTCAGGGACAGACAGTGTCTTCTCCGGAAACTCACCAGCAGCTGCCAGAAATCGAGTCGTCTACATTAT
 CAAGCAGGCCCTCTGTTCCCTCGGATCGGAGCAGCAACATGA

>ORF40709c (SEQ ID NO:422)

AGCCTCTGTTGACTTCATTGTTGCTGCTCCGATCCGAAGGGAACGAGAGGGGCTGTTGATAATGAGAACGACTCGA
 TTTCTGGCAGGTCGCTGGTAGTTGCGGAGAAAGACACTGTCGCTGCCCTGACGTACCAAGAACATGACCGCGAGTCC
 TGGTGTGGACACGGTAGGGCAAGCGATATGTCGCCATCGACTACTACCAAGACGGCGGAGGATGAAACATCCTCGAC
 CACGCCACATTCTCGAACGTATTGTCGACTCAAGGAAAGGGTGGCAAGCCAGAGCTAG

>ORF40507 (SEQ ID NO:424)

TCGATGGGAGACATATCGCTTGCACCGTGTCCAACAAACAGGACTGCCGGTATATTCTGGTACGTCAAGGGACAG
 ACAGTGTCTTCTCCGGAAACTCACCAGCAGCTGCCAGAAATCGAGTCGTTCTACATTATCAAGCAGGCCCTCTCGT
 TCCCTCGATCGGAGCAGCAAAATGAAGTCGAAACAGAGGCTTCACCTCATCGAGTTGATGATCGTAGTAATCAT
 CGCTATTCTGCTGGTATCGCTAACCCAGCTACGACAAATCGTAAGCGCAGGATCGCACCGAAGGACAGGCATTAC
 TCAGCGAAGCAGCCGCTACTCAAGAGCGTATTTTCACAGAACAAACTTATATCACTACCCAAGCCACATGGCAAG
 CTGCATATGCCAACACATGGCACCAAGTGAAGTCCTCCACAGGAAATACAGCCTTACCGTCGATACGGTAGCCAA
 CGACGGAGGTTATCGCTTATCGTAA

>ORF41275c (SEQ ID NO:426)

GTGGGGGGCGTCGGAAGAGCAGGAACTGGAGGGACGGGAGGAACATTACCTTCTGATGCCAAGGAACGTGGGTCA
 AGGCTTTGTAATCGGAATTGGCGCACCTGAAAAGCCGGTTATGCCGGCTTTGCCCTTTCTGCTCTGGCGCTT
 TAGGCCAGCATTGCAACGCTTCTGCTTCAGTCCGGCTTCTGCCGTTGGCGTCAAGGTAGGTTGCCACA
 ATCAAGATCGTTGAATGCCGGTAGCGATAAGCGATAACCTCCGTCGTTGGTACCGTATCGACGGTAAGGCTGTATT
 TGCTGTGGAGGACTTCAGTGTGGTGGCGATGTGTGCGATATGCAAGCTGCGATGTCGGCTGGGTAGTGTATATAA
 GTATTGTTCTGTGA

>ORF42234c (SEQ ID NO:428)

TCGACGTCAGCCGGCTGAACCGTCGGTCGCGCCCTTCCAAGCGGGGAGGGCGGTAGCAAGGTTATTGTC
 TCACCGCGTCGCCACGAGACCACGAAATCAAACCTGCCAATCCCCGGCTCTGCCGGCGTGGATCGGCCA
 TCGAGATCGCAACCGTGCCCTCGATGTCCTGCCGCGATCTACGTGCGTACAGGTTGGTCACAACAAGTTCGTC
 GTGGACAACCTGCCAGCGCGGCCATCTGTCGAGGAACCTGATCAGGTGCCGACAACGTATCGTATCTCAG
 CGCCCAAGCGTTCCAGCGGTCCGCAAGGAAGCCGAGGGCGCCGCTGAAGGTTTCGACGCGACCTGCCGCTGG
 TGACCAAGGTGACATGGAAGTGGTGCCTACAGCCGAGGCCAGCAATGCGTGTGATCGGGCATGAAGGCCACCC
 GAGGTGGAAGGCACCATGGCGAGTACGATGCCAGCAACGGCGTGGCATCTACCTGGTGGAGGACAGGGCGACGTC
 CGCGCTGGAGGTGCGCAAGCCGAAGCCCTGCACTACGTGACCCAGACCACCTGCGATGGACGACACCTGAAGGTCA
 TCGATGCCCTGCCGCCAGTCCCGAGATCCAGGGGCCGCAAGAACGACATCTGCTATGCCACCCAGAACCGCCAG
 GATGCCGTGAAGGAACCTGGCGACCGATGCGACATGGTCTGGTGGTGGCAGCCCCAACAGTCCAACCTCAACCGCCT
 GCGCGAACCTGCCAGCGCATGGCACGCCGCTACCTGATCGACGGCGCCAGGACATGCAACGCGGTGGTCGACG
 GTGTGCGTCGACATCGAACATACCGCAGGCCCTCGCGCCGGAAGTGTGGTGGCGGAGTGTGATCGCCAGCTACGTGAG
 TGGGGGGCGTCGGAAGAGCAGGAACGGAGGGACGGAGGAGAACATTACCTTCTGATGCCAAGGAACGTGGGTCAA
 GGCTTTGTAA

>ORF41764c (SEQ ID NO:430)

AGGCCACCCCGAGGTGGAAGGCACCATGGCCAGTACGATGCCAGCAACGGGGTGCATCTACCTGGTGGAGGACGAGG
 CCGACGTCGCCCGCTGGAGGTGCGCAAGCCGAAGCCCTGCACTACGTGACCCAGCCACCTGCGATGGACGACACC
 TCGAAGGTCATCGATGCCCTGCCGCCAAGTCCCGCAGATCCAGGGGCCGCAAGAACGACATCTGCTATGCCACCC
 GAACCGCCAGGATGCCGTGAAGGAACCTGGCCGACCGATGGCGACATGGCTCTGGTGGCAGGCCAACAGTCCA
 CCAACCGCCTGCCGAACCGCCAGCGATGGCACGCCCTACCTGATCGACGGCGCCGAGGACATGCAACGCC
 TGGTCGACGGTGTGCGTCGATCGGAATACCGCAGGCCCTCGCGCCGAAGTGCCTGGTGCAGGGAGTGC
 GCTACGTGA

>ORF41284 (SEQ ID NO:432)

CTGGGCATCACTCCGCCACCGACACTTCCGGCGGGAGGCGCTGCGTGAATTCCGATGCGACGCACACCGTGAACC
 AGCCGCGTTGCATGTCCTCGGCCGCTGATCAGGTAGGCCGCTGCCATGCGCTCGCGAGTCGCGCAGGGTTG
 GAGTTGGAACTGTTGGGCTGCCAACCACCAGGACCATGCGCACTGGTGGCCAGTCCCTCACGGCATTGCGGTT
 CTGGGTGGCATAGCAGATGTCGTTCTGCGCCGCCCTGGATCTGCGGAACCTGGCGCGCAGGGCATCGATGACCTCG
 AGGTGTCGTCATCGACAGGGTGGCTGGTACGTAGTGCAGGGCTCGGCACCTCCAGCGCGGCACGTC
 GCCTCGTCCCTCACCGAGTAGATGGCACCGCCGTTGCTGGCATCGTACTGGCCATGGTGCCTCCACCTGGGGTGGCC
 TTCATGCCGATCAGCACGATTGCGCTGCGGCTGTAGCGCACCACTTCCATGTCACCTGGTACCGAGGGC
 AGGTGCGTCGAAAACCTTCAGGCCGCGCCCTCGGCTTCTTGCGGACCGCCTGGAAACGCCGTGGCGCTGAAGATG
 ACGATGACGTTGTCGGCACCTGATCGAGTTCTCGACGAAGATGGCGCGCTGGCGCAGGGTGTCCACGACGAACCT
 GTTGTGCAACCACCTCGTACGCACTGAGATCGCGGGCGAAGACATCGAGGGCACGGTTGACGATCTCGATGGCGCGAT
 CCACGCCGGCGAGAACGCCGGGATTGGCAGTTGATTTGATGGCATGGCGTCTCGTGGCGACGCCGTGATTGGACGAA
 TGAACCTTGCTACCGCCCTCCCCGTTGGAAAGGCCAGCGACCGACGGTTAGGCCGGCTGGACGTCGA

>ORF41598 (SEQ ID NO:434)

CCTTCGAGGTGTCGCCATCGACAGGGTGGCTGGGTCACTGAGTGCAGGGCTTGGCTTGCACCTCCAGCGCGGC
 ACGTCGGCCTCGCCTCCACCAAGGTAGATGCCACCGCTGGCATCGTACTGGCCATGGTGCCTCCACCTCGGG
 GTGGCCTTCATGCCGATCAGCACGATTGCGCTGCCGCTGTAGCGCACCACTTCCATGTCACCTGGTACCA
 GCAGGGCAGGTGCGTCGAAAACCTTCAGGCCGCGCCCTCGGCTTCTGCGGACCGCCTGGAAACGCCGTGGCGCTGA
 A

>ORF42172c (SEQ ID NO:436)

CAAGGTTCAATTGTCATCACCGCGTGCACCGAGACCGCATGCAAATCAAACCGCAATCCCCGGCTTCTGCG
 CCGCGTGGATCGGCCATCGAGATCGTCAACCGTGCCTCGATGTTGCGCCGATCTACGTGCGTACGAGGTG
 GTGCAACAACAAGTTCGTCGTCGACAAACCTCGCCAGCGCGGCCATCTCGTCGAGGAACCTGATCAGGTGCCGGACAA
 CGTCATCGTCATCTCAGGCCAACGGCTTCTCCAGGGTCCGCAAGGAAGGCCAGGGCGCGGCTGAAGGTTTCG
 ACGCACCTGCCGCTGGTACCAAGGTGACATGGAAGTGGTGCCTACAGGCCGACGCCACGAATGCGTGTGATC
 GGGCATGA

>ORF42233c (SEQ ID NO:151)

CGACGTCCAGCCGGCTGAACCGTCGGTCGCGCCCTTCCAAGCGGGGAGGGCGGTAGCAAGGTTCAATTGTC
 CACCGCGTGCACCGAGACCGCATGCAAATCAAACCGCAATCCCCGGCTCTGCGCCGGCTGGATCGCGCCAT
 CGAGATCGTCAACCGTGCCTCGATGTTGCGCCGCGATCTACGTGCGTACAGGGTGGTGCACAACAAGTTCGTC
 TGGACAACCTGCGCCAGCGCGGCCATCTCGTCGAGGAACCTGATCAGGTGCCGGACAACGTCATCGTCATCTCAGC
 GCCCACGGCTTCCAGGGTCCGCAAGGAAGGCCAGGGCGCGGCGCTGA

Fig. 3-38

>ORF42233c (SEQ ID NO:151)

CGACGTCCAGCCGGCTGAACCGTCGGTCGCTGCGCCCTTCCAAGCGGGGAGGGCGGTAGCAAGGTTATTGTCCAAT
CACCGCGTCGCCACGAGACCGCCATGCAAATCAAACCTGCCAATCCCCGGCGCTTCTGCGCCGGCGTGGATCGCGCCAT
CGAGATCGTCAACCGTGCCTCGATGTCTCGGCCCCGCCATCTACGTGCGTCACGAGGTGGTGCACAACAAGTTCGTCG
TGGACAACCTGCGCCAGCGCGGCCATCTCGTCGAGGAACCTCGATCAGGTGCCGGACAACGTATCGTATCTTCAGC
GCCACGGCGTTCCCAGGCGGTCCGCAAGGAAGCCGAGGGGCGCGGCCCTGA

Fig. 3-39

>ORF2 (SEQ ID NO:3)

SPIQCQGVPQSEPTHGCRGRHCQAPGRRREQHQYRLQRQRHQLRDRNQQQLGPQQHPLRRRQRHPAVDEQVVRGGLRR
RLRAARCAGRSASRSATGDRL*

>ORF3 (SEQ ID NO:5)

RRSNAKEYLGNQSLTAAAGAGIAKLLADENNTSTVSGNGTSFGTTGTNSNSALNSILSGGVSDIRQWMNKLYGEAFAA
VYVQPGARVAVHLDQQLAIDYELKGRKVDYSSGAAHATADLD*

>ORF602c (SEQ ID NO:7)

SAWSFAEASCCGSIGRSVCLASRSSLRPLLPIELVAPRSQTSSMLASPWGSISSSLVEHAARVSAQARPAQRRRRGLVQ
VCCCMMSGRAVIDLAALFIVDROLLEMHCDPRTWLHVDGGEGLPVQLVHPLPDVADAAGEDAVEGRVAVGSGRPEAGA
VAAEDGTGVVLVGVQELGNAGPGSRE*

>ORF214 (SEQ ID NO:9)

TSCTGRPSPPSTCSQVRGSQCISISNWRSTMNSRAARSITALEPLMQQTWTNPLRLCAGLACALTAACTSKEEMLP
HGEANMLDVWERGATSIGNSRGRLLDARQLRPPIDPQDASANDQADYTRTASNEIHSQFKRLPNPDLVMYVFPHLA
GSDPAPVPGYTTVFPFYQRVQYAMPGERTEDY*

>ORF1242c (SEQ ID NO:11)

SRPGRRTGQSRVFRARRRSAGLLSMRPGRSASNWDRGPRCPRAPVRRMRRANAHPGASLARRAGTQPRAGLRTMGR
DRRGVTLRPAWRHSCSRCWAEEYPWRPVAPDSAQSLLPRPLRPALLNRLERLPVPTEAVCDRAEGFEKSPSIVLRAFARH
GVLDLVEGEHGGVARYRGGIAAGQVREHHQVGIGQSFEITVDLVAGRAGVVGVLIRGGILLRIDWAPQRLPGIEEQP
ATAVAYRAGRTSLPDVEHVGLAVGQHLLLAGGARCQGQRAGQAGAETKKGVSPSLLLHERLQSCNRPCGP*

>ORF594 (SEQ ID NO:13)

PGLRHPHQQRDPQSQTAAQSRPGDVCVPAPGRQRSPGTGLHHRVPLLPASPVRHAGRTHGGLLMGFFQTLLRGRTPQ
QSVPADAPEDSGALDVAEEAETERYLARLAAMGIPLPNTGSKNGATQAEASRLYDHDPSFVDLLPWAELPDEQVMLE
DGRSRAAFFELVPLGTEGRDPNWMQNDARALKEALQNSFDEHETSPWIVQFYAQDEISWDNFQEQLRQYVHPRARGSAFS
EMYLALMHHLEGISKPGGLFVDTAVSKLPWRGQQRVRMVVYRRIRKEDAQIRGQDPAAYLKSICERIQGLANAGIVA
SRMGGQEIRNWLIRWFNPDPDHLGQAEADLRRFYELVCRPDEPILQDELPLADGTFDSQNLFYRQPVSDATQGVWLFDAM
PHRVIVVDQLNKAPLTGHFTGETLKGDGLNALFDRMPEDTLLCITMVTPQDMLEGHLQQLSKKAVGDTQASIHREDVA
TVRRLIGREHKLYRGAIALFVRGRDHTOLEERCITLSNVLLGAGLVPVEPQNEVGPLNSYLRWLPSNFDPNEKRALEWYT
QMMFAQHIANLSPIWGRTTGTGHPGFTLFNRGGAPLTDFPNKLDQMAHGFIFGPTGSGKSASLTNLICQMLAMYLPR
MFVAEAGNSFGLLADLAIRFGLSVHRVRLAPGSGVSLAPFADAALKVESPDQVKVLDAADEIEASDSVQGSKADLEDDQRD
ILGEMEIVARLMITGGEEKEDARLTRADRSARVQAILAAARTCAAANRTVLTQDVRDALYEASRSDSTAPERRARIAEMA
EAMQMFCMGADGEMFNRGTPWPEADLTVDFTATYAREGYAAQLGIAYISLLNTVNNIAERDQFKGRPIVKITDEGHII
KHPLLL PYAMKITKMRKLGAWFWLATQNIIDIPASGAPMLNMIWWLCLNMPPDEVEKISRFRELSPAQSKMMLSARKE
SGKFTEGVLLAKGKEYLVRVVPSSLYLALAMTENEKNQRYNIMQATGCDELEALQVAADLDKARGLPPFPIVFPDQPA
VECQDE*

>ORF1040 (SEQ ID NO:15)

VPARRASDAPGGWFARRILRTGALGHRGPRSOLDAERPGRIERSPAELLRRARNLTDCPVLRPGRDQLGQFPGAVEAV
RPSSSARIGLQRDVPGAAHEASPGGHFEAGRTVRRRRQQAALARTTAPRADGRLPPDPQGGCADSRTGPGGVPEIHLRAY
PRRPGEERRRRFAHGRTDQELVDPVQPPAPGSPRPGGGPTSLRTGMPSGRTDPAG*

>ORF1640c (SEQ ID NO:17)

VRLGLAEVIRVRVEPADQPVPDLSAHARSDDAGVRQAALDTLADGFQVRRVLSANLRILLADPAVDDHPAALLSSPG
QLADGGVDEQSARLRNALQVMLHERQVHLAEGRSSRSRMDVLPQLLEIVPADLVLGVELDNPNG*

>ORF2228c (SEQ ID NO:19)
 GEPAQAVAVQRSDFVLRFDRHQAGAEQYVAQGDAFLQLGMVAAHEQSDRSAIELVLPADQASNGGHVLAGVDRGLGVTN
 GLFRELLQMPFQHVLLRHDHGDAQQRVLGHSIEQGVEAIAFERLAGEVACQRRFVQLVDHNHSVRHGIIEPYALGGIGNR
 LPIEQVLGEVSAVGQWQFILQDRFVRTAYQFVEAT*

>ORF2068c (SEQ ID NO:21)
 SLCSRPIRRRTVATSSRVWIEAWSPTAFFESCCRCPSSMSGVTTMVMHSSVSSGIRSNRALRPSPLSVSPVKWPVSGA
 LFNWSTTITRCGMASKSHTPWVASETGCR*

>ORF1997 (SEQ ID NO:23)
 HPGLDPHPGRGRGHRTSPDRPGAQALSRSDRSVRARPRPVVGTLHHPEQRTARRPGAGRATAERSRTAEQLPALAPLKL
 RSKREASPGVVPDDVRSAHRQPVAHLGAHHRYRTPWLHAVQPWRRAVDLRPVQOAGPADECPRHLRANWLRQVGVPDQ
 PHLPDARHVPAAVVRGSGQQLRPGRLSQAVWPLGPPGAPRPGLRRQPGAVRGRHQAGREPRPSEGAGRRHRLGLGP
 GQQGRPRGRPARHPGRDGRDPRPHDRRREGRCAPDPCRSQRRPGDPGGQDLRRREPHGTDPRRARCALRGLQER*

>ORF2558c (SEQ ID NO:25)
 VGQQAEAVARFRDEHPRQVHGEHLADEVGQGRRLAGASWPEDEAVGIHLPVQLVERVEGQRRAATVEQREARVSGTGGAP
 PDGRQVGDVLSEHHLGVPLQGSLLVWIEV*

>ORF2929c (SEQ ID NO:27)
 SASRTSWVSTVRFAAAQVLAARIAWRTALRSARVRRASSFSSPPVIMRRATISISPRMSRWSSRSALLPWTSEASMS
 SASSTFTWSGLSTSLMASANGARLTPEPGARRTRWTERPNRLAKSASRPKLLPASATNIRGRYMASIWQMRLVRDADLPE
 PVGPKMKPWAFICRSSLLNGSKVNGAPPRLNSVKPGCPVVRPQMGDRLLAMC*

>ORF3965c (SEQ ID NO:29)
 APVGPYQAVDVVAIIHPRALAASAGRYPGDRLPSVESAAPLSVQERISLASAGHPLRGSAGSGSGCRSGSGSANSELSFV
 LAHCRLVWENNGEGWQAAARLVEIRCDLQGRLELVAAGGLHDVVALVLFVFGHQGQVETRGNHTDEVFFALQEHALG
 ELAAFLAGREHHRLRRRQLAEPGULLYFVGHVQAAQPPLDHVQHRRPGWDVVDVLGGEPEPGAQFPPHLGDLHGVGQO
 QRVLGDDVPLIGDLDWPALELVAFGDVHVHQVQDVGDPPELGGVAFARVRCEIHGKVGRLPGRFAIEHLAVGAHAEH
 LHGFRHFGDPRAAFWRGAIAPGGLVERIAHVLGQYRAVRRGGAGPGRRQDRLADGAIGTQARIFLLFATGNHEAGDDH
 LAQDVSLVVLEVGLAALDRVGLDVFGVQHLHLVGALDQLDGVERRQADAGARGEAHPVDRREAKPLG*

>ORF3218 (SEQ ID NO:31)
 GAHHHQAPAAAALRHEDHQDVAETGRLVLARHPEHRRHPSLRGADAEDHRVVVVPEHAPRRSREDIQVPRAVAGAEVDDA
 LGPQGKRQVHRGRAPGQGQRIPRPCGSPELPGPGHDKRKEPALQH HASHRLRARGGLAGRSGSRQGARPAHLPHCF
 PRPTGSGVPGRMRVLNSLTQNLIDNLTQILQNPEEDALQTLRICAPVLIELQQIQLRAVDRRDIVPQIKQLLDEWLQQH
 PQPDTAQQALIEAVDRAEILQRQA*

>ORF3568 (SEQ ID NO:33)
 PTKKKRTSATTSCPKPAATSSRRPCRSQRISTRRAACHPSPLFSQTNRQWSARTNESSEFADPEPDRQPDPAEPRRG
 PADAQDMRSCTDRGAAADSTEGSRSPGYRPAKALG*

>ORF4506c (SEQ ID NO:35)
 VNKFVVFRTFLQSSLVQFRKVQCAARQPAPVAGRLSEDRIDSAPFGAALDPRALHQASLVAAGRLAMHLQGKMAPNQVH
 VRMAVYPALKPRGVDLAEGALQVGVFIDRPARFRIAVEAVVGWQALHQKLYPYGGCSQODQQQPRPGQGGTLKSFGCPAA
 LQESHACLRCRISARSTASMSACAVSGCGCCSHSSKSCFICGTISRRSTALS*

>ORF3973 (SEQ ID NO:37)
 GRGPRGDPTAEASVRLLKGGWAALKRQGPALPWAGLLLVLLAASAVGVELLVKGLPANHSLYGDAKARWTINEYADLECP
 FCKVYTPRLKRWVDSPHDVNLWVRHLPQMHGEARHQARLVECAGIQQGAKAFWSAIDAIFAFQASAGNGGLPGGTLDFP
 ELDQARLEKCAKDNELIDS DIKLDIDIASKGITATPTL VIRDNQ TGRSVKLEGMADETTLLSAIDWLAKDL*

>ORF4271 (SEQ ID NO:39)
 TWFGAIFPCRCMARRPATRLAWWSARGSKAAPKPSGALSMRSSLSRPATGAGCLAAHWTFLNWTRLDWRNVRKTTNLLTQ
 ISSWTSTLHGRRALQRPRPSSSGTTRDEA*

>ORF4698 (SEQ ID NO:41)
 EIGEDSNIPLLVLQDALHFTWQNLDLLPIHNLHYSLVAGAGEAKPQLHCRPSIDVNALEQALHDFDHSLISVSQLHTGIM
 LPRTCRHPYLCTWQRSITARKNTPPTS*

>ORF5028 (SEQ ID NO:43)
 FPAALSEVILSAVCTFLEPVQTHASSLPPWAATNAGRWRTTGTAEQRESGRNLGHHRQGSSGLCHRIVARSVSGRPGT
 PRGATDCGLAPGSTACSSGV*

>ORF5080 (SEQ ID NO:45)
 NRYRPMPLHHSPPGRRPPTLAVGVLLVLLSSASQAETWVITDKAHPVSATGSSRVLFLDAQEELLEEQLTAALPQDPQHAQ
 AAFKRLLQSPDGRLQAEVKAQQDVADAWSLGVEKIPAVVVDRQYVYGEPDVSRALELIAKARRSR*

>ORF6479c (SEQ ID NO:47)
 FVSVSLLEVGTADEHPLALAAVGVT PERPGVLPVDGLRLRPRVGKRAVEAQGWGQLLPFPGRGIALFQLARRPVAVLG
 GCAHGEVDVELADSRGDIAGALGDDGCRLVVGLVQEAAARIEVPPHVAGEDSTHLAQPWDQRFGVHLLGNSMPPANGVQ
 CAEKVRHQDRGGARANVPRGAGEPAERGATRMADHIRFLEAADAVGLVVCGRVIAGLGEWIRCTQRRYLGPGVAPGIRV
 AGDDCVRHVVADLDRRLHFAAMRAAEQPVTDPPDLVFEALRGKGDDGSAVDRGRGREREAEGGGRRCQAAEVEAGHQR
 DLLALAISSRARETSGSP*

>ORF5496 (SEQ ID NO:49)
 ANRQGQEVALMTSLNLLRRAAAATFSLFTASAAINSAAIVSSTLSPQCLEYKVVGICYWLLCGPHGCKVTKTSVKVRHY
 VPDAVVSSYANTGSNPWTEVSALGTPNPLAQAGNDATTNYKAENSIGRFKEADVIGHPGGATFSRFASASGYVCPGATVP
 LVPYFLSTLDAIGWRHGIPEQVYPEALVPGLEVGIFSGDMWGNLYPRSGFLHQTDYKTAAVIAQRAGDITTRIGQLH
 VYLPMRAAPKDGYWPAGELKEGDASTGKWLTPSLNCAVFPNSGPKTQAVDGEHAWALWRPYSCCQRKGQMFCSTD
 FQ*

>ORF5840 (SEQ ID NO:51)
 RDHKLQGREQHRLQGSGCDRPSWWRHVQPVQRQLWVRLPWRHPPAGAVLSQHTGRHWLAWSRAGVPRSGPRAARG
 WNLLRRHVGEPPLAQRLPAPDERRLQDGSRHPARRYHHANRPAPRLLPQGADVHLQYRLPIRTRRIMRMNITSVALMWLLAQLAQADDPIN
 PEPQLRGVSQLWAEDASRRRGARL GALASLLLLPAQGADVHLQYRLPIRTRRIMRMNITSVALMWLLAQLAQADDPIN
 VSKTGTVLSDEVLYSIGGSAVSMGSAGQMDSIGVGFGWNNDMMCGMMNLSTTLENLQNGATQGFQNIQMSVIQNA
 TGAQMSLPALIIQRANPQLYNLITNGIILQARIDYDRSKGTCKTIAEKMADIAGEQTGWGKIAEGQALGATLASDGKDAV
 SALEAVEKKGGNDGVTWVGGDKAGGSGQKPIRIVNDVTRAGYNLLTSRSVNDSSVPSATCNGGLVCNTWSSPQ
 QAAAFATRVLGEQQQTCEGCQKTVTAAGVGLTPLIQETYDKLQLSLSKSKPLTAENLAAAGTDALPITRGVIEALR
 DERDQDVILARLADVSLSMDVLSKALLQLRMLFAGAKEPVAANGLATQAVDQTSLLQQEISNLKTELELR
 RELASNPMRVIERGQQRASGSSGVFESAPDADRLDRLQAPSAGGKSGGRP*

>ORF5899 (SEQ ID NO:53)
 SAILVAPRSAGSPAPLGTALAPPSRWCRTFSAHWTPLAGGMFPPSRCTPKRWSQGCARWVESSPATCGGTSIRAA
 SCTRPTTTRRQPSSPSAPAISPREASSTSTSPCAQPPRTATGRRAS*

>ORF6325 (SEQ ID NO:55)
 ASTARCFPTLGRKKPSTGTPGRSGVPTPAASARGCSSAVPTSNKDTETNHANEHHLGRANVAARSATCPGRRPDQRV
 QDRHGAQRRGPLQHWRQQCGEHQRRPDGLDRRLRLEQRHDRVKEPEHHPGEPQRCHTGFPEHHGLSHPERDRRGHV
 AAGVDHPAREPSALQPDHQWHPAGADRLRPLERDLQNDRKDG*

>ORF7567c (SEQ ID NO:57)

QCLAEHVHQGDIGRQAARQDVLVTLVAQRLLDAAGNWQSIGAGRSQVLCSQWFALRQQLLQRLELLVVGLLDQRGEADAS
 SRHRLAAFAGLLLLIPQYPGGECCGLLGGGSVADQAVVASGGRHARRIIRHAAQGQVVARPGHVVDDANGLLAGAAGL
 VSTNPGYAIIVAFLLCFEGGYGVFPVRGQCGAQGLAFGDFPPAGLLASDVSHLFGDRFASPFRAVVVDPLQDAIGDQV
 VELRVRALDDQRRQRHDRAGRVLDD*

>ORF7180 (SEQ ID NO:59)

FVERAFRHLQQRPGLOHLVLPPGRRIRHPGTGGATATDLRLPEDGDGCWRRPHPADPGDLRQEAPVAAGAAVEEQTID
 CREPGCGRHRCSANYPRRHGAARRA*

>ORF7501 (SEQ ID NO:61)

PGRPGAPPGVRCPLDGRAQQGTATAAPDVRRRQGAQRRRQRPGHPSRRSADQPPAAGDLQSQDRTGTPSRVGQQLPHAGH
 RARATTRLRVQWRVRVGARCRSPRSPAGPLCRRRQVGRETVADTLTRKLLGQLLVGVLIVIGLAVVGTLLSLFALNHF
 GGIQGLEAWRQSNYWSLFAWRALLYCALAIWFRQRKELSAHERQRIRRIEILVLLVLLIEFSKAYFRTGGAA*

>ORF7584 (SEQ ID NO:63)

CSPAPRSPTSPPTAWPPKPSISRPAASCRRSPISRPNWNSVASWPATPPCGSSSAGNNAPQGPVACSSRRPMPIASIACR
 PPLPPAASREGDRDGRYAHHPKASRSATGRSADRHTGSGRYAAQSLRPEPLRWHPGPGLAQLLELVRLAGAAVLRP
 GHRLVPAAGTERA*

>ORF8208c (SEQ ID NO:65)

RSCCASRAEVGFAEFDEQDQQQHQDLDPPNALPLMRAQFLALPEPGDGQGAVQQRPPGEQAPVVALPPGLQALDATEVVQ
 GEETEQRTDHQCSDDQHSDQ*

>ORF8109 (SEQ ID NO:67)

AAAHSADRPAGAVAGPAHRIQQSLPHGRRSMTFMTNDYLEYYLTLLGWIINNGIWNMISDTGLFAVPFAAIVMREWLV
 RGEADEGNKGVLSLARIETHIYGYIVVALAGIPVVNVSFDTIEFDQTRAQQCQYNLPPAPADTGWSSSSLAGKSAQM
 PLWWAMMHALSKGFTSGAIAIPCGBTDLRQMRMEVDNTRVNNPLLAQEIAFSDCYGSPRARLFLMRQPDGLGSAEDNKA
 LQDLNWIGSRFLNTPGYYDTDYSKSPRQSWPYNATRDAGLPQVGGGGGYPTCKQWADSGIGLDRRIKDQVDPDLMTSF
 LKWAKWLQNQDEVTEAVIRQVISPPSSQVKGNVYTDYGGQVGGTVWNGIARTAGTFCVAVGSLAYFPAMDVMVRQALPMVMSF
 LKMMAMVICIPMVLVIGTYQLKVAMTMTVFFAMMFVDWFQQLARYIDSTILDAYGSGSPHLSFNPMGLNTATQDAILN
 FVMGSMFIVLPLLWMTAIGWSGIQAGSVLNGLSRGTEGVQAAGKEAGNRVKN*

>ORF9005c (SEQ ID NO:69)

VSPLLWAGWVAAATTAAHLRQAGIAGGVGVGPRLTGTLLRVGVVVPRGVQQESGADPVQLQRLVVLGDGAQVGLPHEQPRTG
 RPVAVGKISDFLCQQRIVHARVVFHSHLPQIRAARNGRDGAAGEALGQGVHHRPPERHLRTLAGQAAEGARPAGVRC
 RQIVLALLGASLVELDGVEAHVDDRDPRQGDHDVADVDMRLDAGERQHSLVALVGAFPTNFQPFQFAHHDGRERHREQASIR
 DHVPDPVVDDPAEEGEVILQVVICHEGHAAPPVRK*

>ORF8222 (SEQ ID NO:71)

LPGVLPHPPRLDHQQRDLEHDLGYWPVRGAVRGHRDARMAESSWGRRRGQQGSAVSRPHRDAYLRLLHRGRPGGDPRQ
 RELRHHRVRPDSRPAVPIQSAGTGGHRLVELQQPGRQECADAALVGDDARPVQGLHQRRHRGHSVRHGSADANGSGQH
 AREQSAAGTRNR*

>ORF8755c (SEQ ID NO:73)

QSLEKSAISCASSGLFTRVLSTSIRICRRSVPHGMAAMAPLVKPLDRACIIAHQSGICALLPARLLKELDQPVSAAGRL
 YWHCWARVWSNSMVSKLTLLTGIPARATTM*

>ORF9431c (SEQ ID NO:75)

LKPEVDEHHRKEDDRHRHGNFQLIGADDQDHRNADDHCHLQERHHHRQCLADHIHRREVCQAAHRNAEGSCGSRDAVPHG
 AAHLPAVIGVDVTLDLAGG*

>ORF9158 (SEQ ID NO:77)

RLHRLRRAGGRHRVERHRENRRNLRRCGGQLGILPGDGYPGPGTADGDVVPEDGNGLHSDGPGRHLSTESCHDDDGRL
LCDDVRRLLVSVSQIYRQHDT*

>ORF10125c (SEQ ID NO:79)

VIAGCLPLGARRLMMNAHTNKGFASRIGFGLGMLVRFCLHDRRPALRWVKRVSLFLLVALVVSQNFMWLAGVSMTLLCVF
LVGFALVKGDISVSKGSPSRDVSTMTSQAETESVAELFDYQAAHHYRD*

>ORF9770 (SEQ ID NO:81)

SNSSATDSVSACEVIVETSRLGDPLETEMSPLTAKPTRKTHSRVIDTPASHIKFCDTTRATMKNRLTRLTQRRAGRSC
RQKRTSIPRPKPIREAKPLLCAFIINLLAPKGRHPAITYTPKKMIWQALWHIMPLAICRLEYLMATRNVLVPDPLEQDI
NELVETGRYQNRSEVIRAGLRLLQQEAQIAKLETLRNATSSGLMQLERGEYDEITSDELAQYLDLGNQASH*

>ORF9991 (SEQ ID NO:83)

SWTAIMQAETHKHTQTKTDPGGKAFVGVRVHHQSPGSQREASCYHLYAEKDDLASIMAYYATSYLPTGVPHGNAKRRPSR
SAGAGYQRAGGDRPLSESQRSHPGRLAPAAATGSPDRQARNPPQRNIQWADATGARRVRRDHQRRRTGPIPRRARQPGEPL
KHGQVPHLS*

>ORF10765c (SEQ ID NO:85)

HLVCRHPVEDEVPGPNLTDIGHRVAVNEVDAAQASSQFTADAAYLLWVCRNCQRRPYECLVTSARGIAEVVGEAQD
IDDVRLGIMRDAVLGHASVARLVAELVEVLGQFVAGDLVLAALQLHQPTGCCVAEGFELGYLGFLQQQAQACPDDFAA
ILIAAGLHQLVLDILLQRLIGKDDVSRCHEVLQSADS*

>ORF10475 (SEQ ID NO:87)

SMAKYRISHDAQADIVDILRFTHNHFGDAARRRYQALIGAALEAVATDPQQVGSISREELGAGLRSIHLVYCHSMPNVGK
VVRPRHFVFYRVATDQVLEVVRLHDAMDVDQHLPQR*

>ORF11095c (SEQ ID NO:89)

SRMQAVVSTNANAWSGGMQSSGQATAIAHQWPWGTCWMFTRSLFVFAGANAALSAFRQALSGRAFTLVNHSLRPSSPPFL
WAICSCYSCSSLGQVLIHGVVKHANHL*

>ORF11264 (SEQ ID NO:91)

TAVRRDLLKLMGCTHIEADYIGGLRCSTAPEGTWVAGFHGPIVDVIDDSAGFFSTHRLALHYPACGLAVDQAIPTAI
HVASPLMHVCIGKVVVISAWMC*

Fig. 4-5

>ORF11738 (SEQ ID NO:93)

EEVIMKLQAYRLQNYRRLRDVVI EISIFVGANNSGKTSAVQGLYSMLRGEVKKFELFDSAALWAEIDAVGRTPPG
 DEDAPKRLPSILLLWFRVGEDDLATAMSLLPSTEWDGKCVGIRVAEPRDAHELVWKFH EKANAAVALAAKRKAA
 GEQAVEAGAEDAAAVVADAGEYKPWESLTKYLTKE LSKEYTFRYYVLDERA FVGYQAREADYEPLPLGKEPGGAIIKLS
 LVRVDFLRAQRHLD P D AGSSDRAE SLSRRLS RFYHRNLEKRGDDHAALKALDTSEKELNFH LKEVFN DTLTRLA LGYP
 GVNNPEIVIR AALDPTTVLQDAK VHYVIPGVASAQLPD SYNGLGFKNLVYMV VELL DLHEQWA EDDKRA PLH LVFIEE
 PEAHLHAQIQQV FIRNVLRLLEDANDHATLFTQLVITTHSPHILYERGFSP IRYFRRVNDQGHHTDVRNLSLFKTGAS
 DAPAREFLQRYLK LTHCDLFFSDA VILVEGNVERLLLPAMIELVAKRLR SALTILEVGGFAH RFQELIAFVGLT LVI
 TDLD SVTVK TDAEKA A A QGAGAEGAVDGDDE DDDLK PFELEDD DEAEPSGKKSKRGSTCHAH VEGAVTSNQTLISW
 IPKKRSMAELWEVTAEOKTLSAEDS SAGVRVAYQTKVSVT GATTSQLCGRTLEEAFGLENADWCQAEANRSVGLKLKR
 APSSPEELA EKLHDRVVGK NFDKTRFALEVLASGPLNGWKV PAYIAEGLAWLEAKVAHELEADAAIATEVATIEPTTADV
 VAIIVDPGQTA*

>ORF12348c (SEQ ID NO:95)

RKVY SLLSFVRYFVRLSGQGLYSPASATTAAASSAPASTACSPAALRLAASATAALLAFSCSSWNFQTS SWASRGSNAT
 RIPTHLPSHSVLGSSDIAVARSSSPTRNQR SKSM DGNLLGASSSPGV LPTASIAHS AALKSKSSNFFTSPRSIEYRPW
 TADVFPLLAPTKIEI SSSSMTTSRSRR*

>ORF12314c (SEQ ID NO:97)

GTSSGFLAKACTRRH RPPPQPLR PPPQLAPRRPCA WPQARQLRCWPSH VVHGT SRRARGHPEARTLPGS RRTCRPTQC
 SAAAT SQWRGRLHRRGTRDPRVWTVTFWAHPHRQASCRPHRSRPTA P*

>ORF13156c (SEQ ID NO:99)

RQIAHIRVMAQLVVDAEVPNGRESAFIEDVRGVRGDDEL RVEQSRVIVSILKEAQNVPDE D LLDLRVQMLRLLNEDQM
 KRSSLVILGFPLL VQVEQLNHHVDQILEPQ AIVAVWQLGGSYARDHVN LGVLPQD SGR IQGRPNHDLRIVDARIAELGQ
 AREGVIEDFLQEVQ LLLRG I*

>ORF12795 (SEQ ID NO:101)

LPPNCQTATMAWGSRIWSTWWLSCSTCTSSGKPRMTSELRFI WSSLR RRICTR RSSR SSSGTF CASL RMLTITRCST
 RSSSSPRT PRTSSMNADSR PEGT SAA STT SWAITRMCAICRYSKRARP TLQRANS CSGI*

>ORF13755c (SEQ ID NO:211)

ATRTPALESSASDSVFCAVTSQSSAIDRFFGIQLMRVWLDVTAPSTCAWQLP RFLDFLPLGSASSSSSSKGFRSSS
 SSSSSPSTAPSAP CAAFSASVLT VTL SR SVM TSVSPTKAIS SWNRCANAP PTSRMVRAEERRLATNSIIAGRSRR
 STLPSTNITASEKKRSQCVSFYRCRNSRAGASDAPV LNSDRLRTS V*

>ORF13795c (SEQ ID NO:213)

CRRTHRHRNLGLVSYPNPSAGILSQRQLLRRDFPELCHRPLL RDPAD EGLVGRDGT FHVC MAGAATLLG LLLATRFCF
 VVF KLEG LQVVVL VLVISVNGALSACALRG GLLGVRLDRH A VQIRDQ CCEPNEG DQLLEPMRERTTDFKD G*

>ORF14727c (SEQ ID NO:215)

QEVGEKDVLVAKYALGVVTAH A VVERPDAGHSLQASD ISLLVGLPVARGLPDTRAVILELFFKFGDPPADVVLQPNLD
 VGLERLCNRPVKAVDGRDMNQ RVIVDVRQDFIGGKVGIRDADYLLPRPHAGAVL RDHPVQRLDEGGGLAGTC ASTNHEG
 LRRR RYNA CVDLAVGVGIWAINSSAHAVCPGSTMIA TTS AVGSIVAT SVAMAASASSSWATLASSQAKPSAMYAGTFQP
 LSGPLASTSSAKRVLSKFLPTTLSCNFSASSSGLL GARL S LRPTDRFAS AWHQSAFSRPKASSSVR PQSCDV VAP TET
 LVW*

>ORF13779 (SEQ ID NO:217)

RWVRRHHSSAAHRLRPLV LRTGARL RQ TGRSASSSSA HRAALKSWLRSYTI GWSARTSTRPALR WRYSQAGRSMAGR
 FPRTSPRAWPGSKPKWPTSLRMLPSPPRSRLSRLQPM LSL LTRGRRHEQTN*

>ORF14293c (SEQ ID NO:219)

GRWSCRNLRQHEPRAAEASLQCMRGSRRRYLGYQFVCSRLPRVNNDSDNIGCSRNLNSRDLGGDGSIRLKLVGHFGF
EPGQALGDVRGNLPAIERPACEYLQRKAGLVEVLADHPIV*

>ORF14155 (SEQ ID NO:221)

PGADGMSRIDSPDTADREIHACIVATPPQPFVVVRAGAGSGKTTSLIKALDWVISEHGASMRARKQIVACITYTDLATN
EILADVNDDPLHVSTIHSFYWSIAKTFQADIKVWLQNDIRRISELEEEFENYSSVRQTTDRNKADQERYVRSLEAV
AGVRTFNYGVGSDYAKGILGHEDILQLADFLLQNRPFLRRVVALSYFPVFIDESQDTFPGVVKSFKVEAQMQGKFCCLGF
FGDPMQSIFMRGAGDIQLEDHWRAITKPNFRCAKQILDVANAVRAQGQDGMEQVRGLHERVDGNLKLVEGSARMFVLPNT
LNRTEALARVRAWSSATNNDEGWTPDIAVKILVIVHRMAANRLGFGGIYSALNDKTS DAMKQGMQDGTGWPVRPFLSFA
LPIVAAVKAGNEFAAMSLREFSPRLAPAALTGRRAADVLRELHAAASRLVAMLDEAGTTIGDIALHLCDTGLFEDERY
ARVLGFVRDIADTAQEPEAADAVPAEGLSLDATMAKFFNCASQELWPYERYVSEGSPYATQHGVKGAFERVMVVMDEEE
SDYRTNYERVFASAEARAADRALARALGDENTWSRTLRLYVCCTRAQRLVLAFFVADPATLENVVASGILPRSAVFT
QEVLVGWP*

>ORF14360 (SEQ ID NO:223)

SRASRIPTLPPMKSWRSTSTMTRWFMSRPSTAFGTLLQRRSRPTSRCGRTTSAGGSPNLKKSSRITARVSGRPRATGTRP
TKSDMSEAWRLWPASGRSTTAWAVTTPRAYLATRTSFSSPTSCYKTARCSDGWR*

>ORF15342c (SEQ ID NO:225)

EGSNGPTGAVLHPLLHGIRRLVVQRRVDAAEAKPVCGHAVHDDKNLDCDVWGCPTLVVVRRAPRSDSCQSLGSVQRVRQ
DEHPGRPLHQLEVPIPDLVQPADLLHAIALRAHIGIGDVKDLLGAAKVLRLDGPPMILKLDVPCASHEDRLHRAEKTKA
ELALHLGFHFLERLHYTRERVTLIDKHERRVAQRHDPSEQRAVL*

>ORF15260c (SEQ ID NO:227)

MPPKPSRFAAMRCTMTRILTAMSGVVPQSSLFVAELHARTLAKASVRFSVFGKTNIRADPSTSLRFPSTLSCSPRTCSMP
SPCARTALATSRICLARQKFSGFVMARQ*

>ORF14991 (SEQ ID NO:229)

RRQCRAAGRWHGASPRAAREGRWEPQAGGGVGPDVRLAEHAEPNRGFGKSPSVELGDEQRRGLDNPRHRSQDSCHRAPH
GRKPAWLRRHLLGAERQDVGCHEARDAGRHLARSTLPKFCATDRCSCERQ*

>ORF15590c (SEQ ID NO:231)

RSSNSKRPVSQRWRAMSPMVVPASSSMATSLDAACSSRNTSAARRPVRAAGARRGLNSRSRLIAANSLPAFTAATIGSA
KLRKGRTGQPVPSICPCFMASDVLFSAE*

>ORF15675c (SEQ ID NO:233)

SFGRNCISLGLSGVSNIPDKPKNTRIALVELKKTRVTEMESYVTNGGPCLVQHGDKPRRSSVQLSQYIRGTSAGQSR
RQARAEFPEQAHRELIAGLHSCNDR*

>ORF16405 (SEQ ID NO:235)

IDSLRKCVGSLEKCCFACKEIIHVHAIRCRQCGESQGWRRFMSSPTSVVALVLSLLSIAATKPVERLFDAQRAELQISIT
GGDYKAAQLMLTNNGSKPATLVSFEITSKATTNTKTWFLVSNTDGEILEPGKTYKIRASTDESIPKIVEAERRTILKSQY
ALADNCELTAKYIEATGQKVVVRVQPFMCDTPPEKGGLPPGKPGIPIWYLGQE*

Fig. 4-7

>ORF16925 (SEQ ID NO:237)

RPRGRRLCVCNRSCATHLLKRVACPLVNAYPFGTLVKNDVFMPWPALTPIKQSCVRSSNTSLAQLNDCYVYGCCRYVIP
WPYAYEVNSESVQWTIFLLGVDCSGKVIYFRNTARVGPFLAASIYRPWYGSDALVLHFTK*

>ORF17793c (SEQ ID NO:239)

AKMIVIDKNEHLVAQCAICEKTLFDEFSLKIQLGHTYYEPKSLPASASIVYGSHPAPSTFFLEPKIEQQNLVLKSGEQV
ITCSKHYKIPLDYFGLVQTKGTLARLFVQVTCNDGQVEPGFDGYVTLEIVNMSPWTIEIPAVSDIAQLYLVKCSTSASE
PYHGRYMDAAKKGPTLAVFRK*

>ORF18548c (SEQ ID NO:241)

RTMAGWPRLAAQGRRTNLMSVLQIKGRTTKSHTFDAASYSSNSLILTDAGDERIEEPSLELSVGEWSDNYSGNDKNLW
RIVDGMTIRGHDSVVVEAAEIKVPHNRYGIVLPTGSLFLSRGVLVASAKVEPAFDGKLKLRIFNTTNKNVCLTKGEKLG
SVIFFSTESTHTQSPIKRGSEISTLPITRRARLKKWFSLNPTIWVGWTLNLIGSSLVSSLIMYAVYYKVVLEHQSQPPQS
QQNAQPSNEVKPK*

>ORF17875 (SEQ ID NO:243)

TAYIIREDTRELPIKFSVHPTHMGLSENHFNRARRVMGSVDISLPRLMGLWVCVDSVEKKITEPSFSPLVRQTFLVV
LNILSLSLPSNAGSTFAEATSTPRERKRLPVGRTMPYRLCGTLISSAASTTTE*

Fig. 4-8

>ORF18479 (SEQ ID NO:245)
 SVTHSSDLSFVLGLRDAATLPLSFI PADIPGYRLKDDVRKACTNLNFKRLAVIGERERHRPYITWRQHTGTERYPASEQ
 RASRKKKRQIFRQIEFFH GARQISLARFHDEAVIRVCEHDLA RGASRRFSQASTPYCQAREACESEVKSNAFRGGQLT
 VGKVLD*

>ORF19027c (SEQ ID NO:247)
 MIYSPHSLLKLVRDGKLIKHLAHRELTTPEGVGFDLRLAGLSRLTVGGSLRESTRRTPASEVVLADPDDCFVMEPGKTY
 LASTMEEFDLPEDLAALFFPRSTLFRSGITFSSSVLPPGYVGPMTFALTNNHSEAFEIQIGARFAHVIFQAVSGDIGRYK
 GQWQGGRVSQPKDEGQI*

>ORF19305 (SEQ ID NO:249)
 WPFSACRLFGMTGQVGCKRWSAPMQLGGHVRCNYAVEPGPVPPKQSIRPRWHIANKIPFPATVVLSSLPAIWRKSPLHE
 SSWSLPCFNSFPGYPGSRPPPQQPKLPQGDSSFL*

>ORF19519 (SEQ ID NO:251)
 SGGKARSMNRHGASHVTPFLDIQEAVPHPNNQSCP RGIHPSSEQHGTARHASPPAATGEHLAARLAIQAAIRGDLPAAT
 GQLC RAGPAAPCFGKSPCPSSRRDRSRPGDRGLRTQGTADLPAPDRRSAGVTVSPG*

Fig. 4-9

>ORF19544 (SEQ ID NO:253)

IVMEPPMFQLLSWISRKPSPTPTKAAPGGFILPLSSMELLGTPRRQLENIWQRASLSKQQFEEIYRPLANYAELVQ
 QLPASENHHAHPGMIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAYGALAHIGKIVVDLQVELQDG
 TWHPWNGPINQPYRFKYVKSREYQLHGAASALLIHQLLRTALDWLSRFPELWAQLIYLFAGQYEHAGILGEIIVKADQA
 SVAQELGGNPDRALAAPKQSLQRLADGLRFVVKDFKLNQPSGSDGWLTDALWLSKPAADQLRAYLLAQGIDGVPS
 SNAPFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRNFKTLLKIAPALIWTDAERPSYSGSLVVEDGTASTEKPETTC
 EIPNGPAEQQQAPETKMMHLQPAVSKPANEQKAIAPKSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRG
 EENLQQPLGTTKEPTDCAPEAIEDVFMPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDTGMLVTPGIFKRYQ
 EHPVLEKLAQAKETTGWLKVQRAFEKQGLHRKTSKLNINIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNP
 SLTIVTDA
 EGGVE*

>ORF20008 (SEQ ID NO:255)

ATGRQHLAPLERTDQPAIPLQVREVPRIPAPRRCSTSHPPTATAHCTRLAQSLRAVGSIDL
 PVRWAVRARRDPDDHR
 EGRPGLSCTGARRQGSSSGCTEAVAAAAGRRPSLLGEGQVQVEST*

>ORF20623c (SEQ ID NO:257)

RELVSPSSTVVYRGRPNGLVLGICLDDGLVLEHAEERRVRGGHPIDTLGQQVGSQQLIGSRLAHQPECV
 LGQPSIRRAARL
 IQLELVLHQEAKAVCQLPLQRLRCSQSSIRIAS*

>ORF21210c (SEQ ID NO:259)

RLKIPGVTSMAVPSTVCTKALVSLMNRRRAAMPDFIQPTN
 PCPRSVLLGINTSSI
 ASGAQSVGSLVPSGCCRFSSPRVF
 VGEAAGESWLVS
 SSSSGELILPRSAKSSVSS*

>ORF21493c (SEQ ID NO:261)

AAAASFHTSGIGDDREAWVVQRLLREQQF
 GILEQVGLELFRLARTRNLDGPDVQVFTGLPMKPLFFERALHQLPAGRLL
 GLGQFFKHRM
 LLDIALENSWRDQHGGPVYGMHQSLGVV
 DEQATGRDARFHPTNESLSQ
 ISTSARHKYIFNC
 FRS
 AICWLL
 GP*

>ORF21333 (SEQ ID NO:263)

TSGPSRFVLARRKSSRPTCS
 RIPNCCSLSLWTTQASRSSP
 MPKEVWN
 DAAAHRGVHLRARS
 PGSQREDL
 PRRDQGAA
 QALRSYGNRTGRGPP
 GCPGMATQGTGTRPV
 QAELEH
 VLESSADDLGLCHRA*

>ORF22074c (SEQ ID NO:265)

VRHKPLRYWHYELFV
 SLLCLAADEDQ
 LIFPV
 DVALADAQ
 QRIQPD
 AGEVEDL
 KRAKPE
 PGG
 RDPC
 AFAGA
 ALCAV
 LHEP
 IAGEQDG
 FGG
 DGF
 ACSP
 GGN
 DGG
 LSER
 VDL
 GVR
 HQ
 LMD
 GIA
 PDR
 PQM
 IRV
 RV
 PAP
 LGQ
 ALF
 QYL
 ASP
 SQD
 SP
 VV
 HLY
 G
 CRR
 TEV
 LEQ
 RL
 GAV
 DLR
 AGF
 PEI
 VRE
 DVL
 LGE
 LLR
 HST
 PPS
 ASV
 M
 T
 VRL
 GLS
 RG
 CG
 NS
 NLG
 SWSR*

>ORF21421 (SEQ ID NO:267)

AASGQPKPHGHRCRRCGMT
 PQLTE
 YYIF
 AHD
 LRE
 ASAKI
 YRA
 ATK
 ALL
 KHF
 GPT
 ATV
 QDV
 DHRA
 VLG
 WRR
 KVLEQGL
 SKRS
 WNTY
 SNH
 LRT
 IWGY
 AIE
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>ORF20008 (SEQ ID NO:255)

ATGRQHLAPLERTDQPAIPLQVREVPRIAPRRCLSTSHPTATAHCTRLAQSLRAVGSIDL PVRWAVRARRDPRRDHR
EGRPGLSCTGARRQSGSSSGCTEAVAAA VGRRPSLLGEGQVQEST*

>ORF20623c (SEQ ID NO:257)

RELVSPSSTVVYRGRPNGLV LGICLDDGLVLEHAEERRVRGGHPIDTLGQQVGSQ LIGSRLAHQPECV LGQPSIRRAARL
IQLELVLHQEAKAVCQLPLQRL RCSQSSIRIAS*

>ORF21210c (SEQ ID NO:259)

RLKIPGVTSMAVPSTVCTKALVSLMNRRRAAMPDFIQPTNPCRSVLLGINTSSI ASGAQSVGLVPSGCCRFSSPRVF
VGEAAGESWLVSSSSSGELILPRSAYKSSVSS*

>ORF21493c (SEQ ID NO:261)

AAAASFHTSFGIGDDREAWVVQRLLREQQFGILEQVGLELFRLARTRNLDGPDVQVFTGLPMKPLFFERALHQLPAGRLL
GLGQFFKHM LLDIALENSWRDQHGGPVYGMHQSLGVVDEQATGRDARFHPTNESLSQISTSARHKYIFNCFRSAICWLL
GP*

>ORF21333 (SEQ ID NO:263)

TSGPSRFLV LARRKSSRPTCSRIPNCCS LSSLWTTQASRSSPMPKEVWNDAAAH RGVHLRARSPGSQREDLPRRDQGAA
QALRSYGNRTGRGPPGCPGMATQGTGTRPVQAELEHVLESSADDLGLCHRA*

>ORF22074c (SEQ ID NO:265)

VRHKPLRYWHYELFVSLCLAADEDQLIFPV DVALADAQQRQI QPDAGEVEDLKRAKPEPGGRDPCAFAGAACAVLHVEP
IAGEQDGFGGDGFACSPGGNDGGLSERDLGVRHQLMDGIAPDRPQMI RVVPAPLQALFQYLASPQDSPVHVLYG
CRTEVLEQRLRGAVDLRAGFPEIVREDVLLGE LLRRHSTPPSASVMTVRLGLSRGCGNSNLGSWSR*

>ORF21421 (SEQ ID NO:267)

AASGQPKPHGHRCRRCGMTPQQLTEEYIFAHDLREASAKIYRAATKALLKHEGPTATVQDV DRAVLGWRKVLEQGL
SKRSWNTYSNLRTI WGYAIEHELVTHSQVNPFRKTTVIPPRRASKTVAAEAILLARNWLNMQDGAERCTGERARITPAW
FWLCTFEVFYFTGIRLNALLCIRKRDIDWENQLILIRGETEKTHKEFVVPITEGLVPHLSRLLQEADRAGFADDQLFNV
NRFSPHYKS KVMNSDQVEAMYRKLTEKVGVRMTPHFRFRHTLATDLMKAPERNIHLTKCLLNHSNIQTTMSYIEADYDHMR
AVLHARSLAQGALENVKVDYSGSPQASAKPKPCGQPLARVSEAPPPEARTEPAEPREHTPGTGIQGGPTAWEADALPQP
PDTFEP SVLFTLMAQNL SNRAASASAAPAATSGSGGWGSA ARSNLA*

>ORF22608c (SEQ ID NO:269)

RICFPRGWTSLNACPWRVLPWF CRLCPGLR WRRFTHSSERLPAWLRFGRGLRGA AVIHL PDI LQRALGQASSMQHGT HVI
VVGLDVAH RGLDIRVVEQALREVN VPLGCLHQVGGQGV PETVRGHPHPNLLGQLPVHGF DLVGVHH LALVVR*

>ORF22626 (SEQ ID NO:271)

HLRTKRAVHS DGSKLIEPCRLGIRGSRCNKRIRRMGICRPKQSRLAIPVLRAGYRTKGSRAFQQIVRPV GK IWN YRERLD
SSAGMLAEPAQFQGQYHSTLCNR*

>ORF23228 (SEQ ID NO:273)

RDSNSRHPAKAGALPDCAIPLREFGSATWTRDPMINSHLLYRLSYRGTSSFQPWTLPVLLDSRLRGAPFYGCARACQ
 PSDPKSFSSFSTSDFKTAFLHAAALSLRPDAHEKAPPKRGFPCPPPKRSGEDDLVAFHLRRDTGTRREFAGQDQLRQRL
 DPALDGPLQRACAIDRVEADGNQLVQRLLAQFQALQALGQALQATELDLGAGDLLASQRLEHHHFVDPVDEFRTVE
 RIVHHCGTLRLAVAGQQLLDRRTEVGGHHHHGVAEVHRTPVTVQASVLEHLEENVEYIRMGLHLVQQHHRVGLAADR
 GQVAAFLEADVARRADQAGHRVFLHELGHIYPHQRLLGIEEELGQRLAQLGLAHPGRAEEERAARPVRIGEAGARTAH
 GVGHDYRLVLADHSPMQLLHAQQLLALALEHLRHDGTPLGNHFGDFLVGHLVAQQLVLGLAVLVDHLQAAFQVRDGL
 VLDARHALEVALAPRRLHLLGLLDDLLRRLALHLGLLGLPDLLEVGVFALELDILLQLGALPGGFVVFLLQRLALD
 LQLDQATVETIQFLRGVDLHADAAGGLVDQVDSLVRQLPIGDVAVRQLGRGDDRAVGDAHPVVFIAFLEATEDGDGVF
 LARFVHQHILLEALQRGILLDVLAIVLVEGSSTDQLAARQSRLEHVAGVHGTFRLAGADHGQVFVDEQDDPAFLLAQFV
 EDRLQAFLEELAELGTGDQRPVHQGQQLVLEAVRHFAVDDALGQALDDGGLADAGFADQHVVVLGPPLQDLDGPADLV
 ATDHRVELAFLGALGHVDGVLVQRLARLLDVRVHFAATQVGHGILQRLARHALAEQQLAEPGVLVHRCQQYQLAGDEL
 VALLLGQAVSLVEQACEILGQVHVAGRQLRQVEFFVEAAAQGGDIEADLHQQLDRTALLLEQGGKQVHRLDGRMVM
 ANGQGLGVGERQLQLAGQTVYSHGSSFL*

>ORF23367 (SEQ ID NO:275)

AIAERLSSNPGRFRCWIRVSEARHFTDARGHVNPLIQKVFLFPRATKRPFHCMRQRSRAYRTPMKKPRRSGAFPVRPR
 RGQAKTISSPSTFAEILAPGANLPARISCAGFSIQRWMARFSGRAP*

>ORF25103c (SEQ ID NO:277)

SAPRGEHHRRRDHRRGQAVAPLHRSATAGQGHRPDRRGRQPHGDRLQAGGTGSSRSPDPAEDRARGAEEGRRRSHQ
 EAPGQAGGGYRQARARIIRRPGDLEVREGRGAGLGADPAEDRAGQAGDGGAAQGRPREHGAHPVDPHPGPGTQPADGRP
 ARQDREPVAQQGDRRGNRSGFQVDRYGPVEDARGRAREAAAHGAGAASASDRPGRGGSRRVQRRAPFARRPRRSEPAE
 RLVPLPRPDRGGQDRRVQGAGRVLRYRGAGADRYVRVHGETLGGPPDRRASGLRRLRGRRLPDRGDPPQALLGGAAGR
 GGEGPSGCIQHSPPGARGRTPDRQSRAYGGLPQHGGDDLQPRFGADPGAGRRPRGATCRSDRGQCALPSGIHQPDRRS
 GGVRAAGSRADRRHRRDPARSPAQAPGRARAEPGTEPGGAGQADCRLRPGLWRTPAEAGHPALDREPAGATDPRQIRA
 GCQYLGEGGRRRDLRLTSSGADRESPASAGLFHGRPVGARALPHAVEGPFCRSWKKKNFLQRVDMMPARIRKMARL*

>ORF23556 (SEQ ID NO:279)

KSPAEAGLSSLAPPEEVRRRSRRLPPSPRYWHPARICRPGSVAPAGSRSSAGWPASAGVRHPRGRSRRQSACPAPPGSVP
 GSARARPACAGDRAGSRRCRRSAREPAARTPPLRRSG*

>ORF26191c (SEQ ID NO:281)

KEGRPMRIDRLTSKLQLALSDAQSLAVGHDHPAIEPVHLLSALLEQQGGSIKPLMQVGFIDIAALRSGLNKELDALPKIQ
 SPTGDVNLSQLARLNQADRLAQKQGDQFISSELVLLAAMDENTRLGKLLLGQGVSRKALENAVANLRGEAVNDPNVE
 ESRQALDKYTDMTKRAEEGKLDPVIGRDEIRRTIQVLQRRTKNNPVLIGEPVGKTAIVEGLAQRIINGEVPDGLKDK
 RLLALDMGALIAGAKFRGEFEERLKAVNLGKQEGRVLIFIDELHTMVGAGKAE GAMDAGNMLKPALARGEHLCVGATT
 LDEYRQYIEKDAALERRFQKVLDPESEEDTIAILRGLKERYEVHHGVSITDGAIAAAKLSHRYITDQLPDKAIDLID
 EAASRIRMEIDSKPEELDRLDRLIQLKIEREALKKEDDEATRKRLAKLEEDIVKLEREYADLEEIWKSSEKAEVQGSAQI
 QQKIEQAKQEMEAARRKGDLESMARIQYQTIPDLERSLQMVQDGKTEQLLRNKVTDEEIAEVVSKWTGIPVSKMLEGE
 REKLLRMEQELHRRVIGQDEAVVAVSNAVRSRAGLADPNRPGSFLFLGPTGVGKTELCKALAEFLFDTEEALVRIDMS
 EFMEKHSVARLIGAPPYVGFEEGGYLTEAIRKPYSVLLDEVEKAHPDVFVNILLQVLEDGRLTDSHGRTVDFRNTVV
 MTSNLGSAQIQELAGDREAQRAAVMDAVNAHFRPEFINRIDEVVVFEPPLAREQIAGIAEIQLGRLRKRLAERELSLSQ
 EALDKLIAVGFDPVYGPRLKRAIQWIENPLAQLILAGKFAPGASISAKVEGDEIVFA*

Fig. 4-12

>ORF23751 (SEQ ID NO:283)

TGSKPTAISLSSASWLSSRLSSRSARRLRRPSWISAMPAICSRASGSNTTSSIRLMNSGRKCALTAITAARCASRSP
ASSWICAEPRLEVITTVLRKSTVRP*

>ORF24222 (SEQ ID NO:285)

PGGAPIRRATECFMNSDISIRTSASSVSKRNSASALENSVLPTPVGPRKRNEPLGRFGSARPARERRTALDTATTASSW
PITRRCCSSCMRSSFSRSPSSIFDTGIPVHLETTSAISSLRSNWFSLPCWSTICRLRSRSGMVWYWMRAMLRSRSP
LRRAASISCLACSIWCWICAEPCTSASFSDFOISSRSAYSRSSLTISSSLARRFLVASSSSFFSASRSIFSWIRRRSRRS
SSSGLESISSMRMLAASSIRSMALSGSCRSM*

>ORF24368 (SEQ ID NO:287)

TRTYLSAPAPPYRRGTRPAPCTTRSCPPRSGRGRGTSRSAGSDRRGRRANGARRWTRRLPPRGRSLADAAPAPCAAAS
RARPRASSTPGYRSTWKPLRRFPRRSPCCAATGSRSCRAGRPSAGCVPGPWGTGCAPCSRRGRCAPCAAPPPSPAWPARSS
AGSAPSPAPRPSRTSRSPRGRRIRARA*

>ORF24888c (SEQ ID NO:289)

RRKTTKPPGSAWPWRRRISSSSANTPTSRRSGSPRPRCRARRSSRRSSRPSRRWRRGARATSRAWRASSTRPSRTW
NAACRWSTSTARPRTSCCATR*

>ORF25398c (SEQ ID NO:291)

RRSSTNWASRKAGSSCSTNCTPWSAPARRKVPWTPATCSSRLWRAASCTASVLLSTSIASTSRRMPRSAASRCWWT
NRARKTPSPSSVASRNAMKCTTG*

>ORF25892c (SEQ ID NO:293)

PPGPAEGRPVHLQRAGIAGRDPREHQARQAAARPGRAVQGAGECRGQPAWRRSGERPERRGVAPGAGQVHRRHDQARRGR
QARPGDRSRRRDPDPHPGAAADQEQPGADRRRDRQDRHRRGPGPAHHQRRSAGRPGQAPAGPGHGGADRRQCQVPRRV
RGTPEGGPQRTGQAGRPGHPVHRRTAHHGRRQGGRCHGRRQHAQAGSGARRAALRRCYYPRRVSPVHREGCAGAPLPE
GAGGRTERGRHHRHPPWPQGTL*

>ORF25110 (SEQ ID NO:295)

RSLRPRRMAMVSSSLGSSTSTFWKRRSSAASFSMYWRYSRVVAPTCSSPRARAGLSQLPASMAPSALPAPTMVCSSSM
NRMTRPSCLPSSLRTAFRRSSNSPRNLAPAISAPMSRASRRLSLRPGTSPLMMRWARPSTMALPTPGSPISTGLFLVR
RCRTWMVRRRISSSRPITGSSLPSSARLVMSTVYLSSAWRDSSTFGSFTASPPRRLATAFSSALDTPWPSSSLPSLVFSS
IAASNTSSLEMNWSFCWARRSAWLSRRARSWDRFTSPVGLWIFGSASSSSLRPLRRAAISKPTCISRGLIEPPCCSSRA
ESRCTGSMAGWSWPTARDWASESASCSSLVKSIRMGPSFYRAGRNDGCP*

>ORF25510 (SEQ ID NO:297)

CAGPGPWRSCRRVRSAPGCSWSAAAGPGWGGSRRDRSPGRACLPRAWSCRRCTCPAPGATPSSGRSPRLRRHA
GWPRHSPACATRPGRAAACRAWCSRPSRPAIPARWR*

>ORF26762c (SEQ ID NO:299)

PPTACRRCSATARAPGWPRPMPAGAGWRRACWRRWTAWACPATNCWGWGRSARRPSRSAARSAMHSSLTPRRARLS
YLAPIRAASWPTSTDGSAWAPMASPPCMAAASAPSAPIRASPITAARRVPAVLPAWSGRTRPAQVIRQLTDVTVRS
LEPRKIALIY*

>ORF26257 (SEQ ID NO:301)

IRAIFRGSSDRTVTSVSCRRITCAGLVLEPDQAGKTAGTRRAAVGIEARGIAEGAEAAAMHGGDAMGAQADPRESVDVGH
EAARIARYESRARLGVRSDECIAIDLADLEGRLRADRRPQDQQFVAGHAQAVHRLQHARRQPAAGMGRGHPGARAVA
EQRRQAVGGHDRTG达尔RAPAVGVPEHRFGSASTTSLRAPIPTSSAGIPDARSGVGGFIPRRADRRRGQGSDCRRVP
G*

>ORF26844c (SEQ ID NO:303)

RGGGRPEPVLRADASWSAMPVACTIMTADCLPALFCDRSGTRVAAAAGWRGLAAGVLEATVDSLGVPGDELLVWLGP
IGPQAFEVGGEVRAFVAAHAEARSAFVPSANPGRFMADIYRLARIRLGAHGVTAHGGFCTFSDTARFYSYRRSSRTG
RFASLVWLQD*

>ORF26486 (SEQ ID NO:305)

MSAMKRPGALALGTTKAERASACAATNASRTSPPSKACGPIAGPSQTSSSSPGTPRLSTVASSTPAASPRQPAWAAATRVP
ERSQNNAGRQSAVMIVQATPGIALQLASALSTGSRRPPRHSVHLFQPARPAFQTLGQASAVLFH GARIVDVGAKVQTV
EGCLADPATARGHAGPHTGRRPVGGQPGVQPTNASRSWRNRLSSQRNSSGSGDSHFMRTPVAG*

>ORF26857c (SEQ ID NO:307)

VHGVTWWRPTRTGAQGRRQLERDAGRRLYDHDRLPAGVVLRLGHPGGRGPCRLARAGGGRAGGDGGQPGRARRRTAGL
AGAGDRPAGLRRRGPRCIRRCARRGALGFRT*

>ORF27314c (SEQ ID NO:309)

SGNRRCRKNSSGCSACCARIARRSVERLADPRLAGAGPCAGLRDHAQWRGQPGTLLRQSEPWRPRLRRSARRGIKPPTPD
RASGMPAELVGIGARSDVVEADPNRCSGPTAGARCRASPVR*

>ORF27730c (SEQ ID NO:311)

QARRPGGPGSGCRPSGRPAECLALPCPGHRQCAARRDRPPPQGHDRPDGSGQDAGGPHQAGGATAGTVGQPHLRGDRDR
RDHLRRHRCADRTAWAAAEDGGGRRQGGQPLPRA GTLPCAHPYQPGQAGDRAYPPDPRAHEPYWLSPGRRSGLRWA
QDSPGGQPDPGDSSRIPPAGAARALPRTGSPGHRRRAHEVGIAAGRIPLAAQPVAPGSRGVRLNAWLTPDWAPARVR
ACVTTRSGGVSQAPFDLNLGAHVYDDPRAVE*

>ORF26983 (SEQ ID NO:313)

PRHCAWSRRPAHGPAPASRGSARRSTDERLAILAQQAEEQPEEFFRQRRFPLHAHAGGRVIQFEEARVQRLPGEFAKSLDQ
GLAGHGNPPEAPTVDRIAQGIANMAHVADLVGTPGLQIDPGMGVRTEAFQHAVMADRHLAGVDHRHLLPLHAMP SDR
IDGAAGGDHADHDLVDAADRPCLQLRHQLGVGLQRLGHYHQAGRVLVQAVDDPGARHIGDVRDMVEQGIQQGAVL MAGS
RMDHQAGGLVNHQDVLVLDQDQLRAAVDDVARAQHGAVDGQATVLDPAQGTGAGVFGKKL
GGDLVETLATQLERHLGRALNHIGE*

>ORF28068c (SEQ ID NO:315)

PQRVADSKSRAEHRLLLMSDMIQRAAEVPFELGGQRLDQIAAQLFPEHSRSRLAGWIKDGRLTVDGAVLPRDIVHSGAQ
LVLEAEQEAQGEWLAQDIELEIVYEDEHILVIDKPAGLVVHPAAGHQDGTLNNALLYHVPDIANVPRAGIVHRLDKDTG
LMVVAKTLEAHTKLVAQLQARSVSRIYEAIIVIGVITSGGTIDAPIGRHGVQRQKMAVVDAKGKAVSHYRVLERFRAHTHT
RVKLETGRTHQIRVHMSHIGYPLVGDPPVYGGRFRIPPVASQTLVQTLREFPRQALHARFLEDPATGVRMKWESPLPEE
FLWLLSLLRQDREAFVG*

>ORF27522 (SEQ ID NO:317)

PTVPAVAPPACGPPASWPLPSGRSCP CGGGRSRRAAHWRCPGHGRARHSAGCRPDGRQPDGPPGRRACQSPGCARPR
RFPARCPVRATRPGPARPPGPVARCGRCRAGAARRRRSGDRP*

>ORF28033c (SEQ ID NO:319)

ASSPTHVRYDSTRGRGAVRAGWPASRPDRRPFSRTLPLPSGRLDQGRSPDRRRAAPARHRPQRRATGPGGRAGSPGR
VARTGHRAGNRLRGRAHPGD*

>ORF29701c (SEQ ID NO:321)

SSSSLEISRTSTRPMVRRYRWFRRMRCPCSSLRSRSARTVALVLAQVRLAAIPALFVGEVGVLRVDAAMGAADHRRCA
ARLVLRLTLLARSHTGKATPEPERDGDQGDPEQEAKEAHGDLGGWRKLQFQSQAAGSIPDGKVQAVRRLALGEAWRRAKRR
EACASLRCFVRSVEETEGHVAPPGATGVLVIALRLVVGAVILVFRILQFGGDLPLGILVLLDHLVLLGFFHVRRLAASF
DQAQGGLQPGAGVGLAFAGDELAILEAGVIRIVQLEGFQAGAGQVVEIQATVGFHDHQIAIDGRGFLEVLLHVATAVG
GGDIGLALQVVVADVHFVGRQQAQVHHARLGVRGVAAVGEAAGELGELVEGVAGGARVALGHVQRQEARQQAALVVEGG
QAFEVVGVVDVGVLRMQADEFGGGAGGFGHLHVLVVGVDDQLELGLLGVAAEGIARFEGFQLGDGAVVALVVEVLLVQ
LALAQVLVDSLLVRGAGCGEGEDGDDQVFHLHGGLRPWDGRLGLNRLL*

>ORF28118 (SEQ ID NO:323)

QTVEAKPTVPGTQAAMQVKHLLIAILALTAACSSNKETVDENLSESQLYQQAQDDLNNSYNSAVTKLKALESRYPFGR
YAEQAQLELIYANYKNEPEAARAAAERFIRLHPQHPNVDYAYILKGSSFDQDRGLLARFLPLDMTKRDPAARDSFNE
FAQLTSRFPNSRYAPDAKARMVYLRNLLAAYEVHVGHHYLKRQAYVAAANGRYVVENFQETPAVGGLAIMVEAYRRLG
LDDLASTSLETKLKNYPDNASLKDGEFVARESEADTRSWLAKATLGLIEGGEPFPHMETQAAKDVIKQYEDAEREIPAEL
KPNQDHSADEKPESSDDDEDSGRSWWSYMTGLFD*

>ORF28129 (SEQ ID NO:325)

GQADRPRDASRHASETPAADRHPHRSLLEQGDCRREPAREPAPVAGAGRQQQELQQRHQAESPRIALSLRPLRRA
GPARADLRQLQEHGARSRPRRRTLHPPASAAPQRRLRLLPQRPVLLPGPRPAGLPAAGHDQARPGRPRLLQVRVPA
HQPLPQQPLRPGRQGAHGVPAAQPGGLRSARRPLLPEAPGLCRRQPRSLRGELPGNPGRRWPGDHGRSLPSPGSRRP
GQHQPQNPQAELESG*

>ORF29709c (SEQ ID NO:327)

GPDPVWRSAAGPVGRWSGGTGGDGGCVAPAPRSAAVQRARSPWSRRCAWLQYQRCSWARALACGTWTPQWAQRTI
GDALGSSCGRCCWRGVGRVKKRQSQNAMEIRAIQNRRKRPVISEAGESCSLAKPPARSQTGRSRLCGVWRWERHGGGQ
KEGRPAPPFGVSCDQSKRPKVM*

>ORF29189 (SEQ ID NO:329)

SHETPKGGAGLPSFCPPCLSQRQTPHSLDLWDRAGGLAKLQLSPASEITMGLFRLLFWIALIAIAFWLWRRFTRPTP
RQQQRPQDEPSASPMVRCAHCGVHPQANALAHQRWYCSQAHLRQDQGDRAR*

>ORF29382 (SEQ ID NO:331)

SPSRSGSGVALPVPLRASSNVRTSRAHRRWSAAPIAASTCRRPTPSPTNNAGIAARRTCARTRATVRAERLRLSEEQQ
RILRLYHLYRLTIGLVLVLLISSELEDQVLKLVHPELFHVGSCYLVFNILVALFLPPSRQLLPIFILALTDVMLCGLF
YAGGGVPSIGSLLVVAIAIANILLRGRIGLVIAAAASLGLLYLTFFLSLSSPDATNHVYQAGGLGTLCFAAALVIQALV
RQEQTETLAERAETVANLEELNALILQRMRTGILVVDSRQAILANQAALGLLRQDDVQGASLGRHSPMLHCMKQWR
LNPSLRPPTLKVVDGPTVQPSFISLNREDDQHVLIFLEDISQIAQQAQOMKLAGLGRLTAGIAHEIRNPLGAISHAAQL
LQESEELDAPDRRLTQIIQDQSKRMLVIEVNLQLSRRRQAEPOQLDLKEWLQRFVDEYPGRLRNDSQLHLQLGAGDIQT
RMDPHQLNQVLSNLVQNGLRYSQAHRGQVWLSLARDPESDLPVLEVIDDGPVPADKLNNLFEPFFTTESKGTGLGLY
LSRELCESNQARIDYRNREEGGGCFRITFAHPRKLS*

>ORF30590c (SEQ ID NO:333)

LLQQLGGVADRAQRVADLMGDAGGQAQKTGQLHLLRLGDLRVFEEDQHVLVVFAVEADKAGLHRRAIRHHLERRTEA
GIQAPLLHAVHQHRAVAAEAGALHVLPQEAEGGLVGEEDGLTAIDHEDAGAHALQDQCVEFLQVGDRLGAFFGQRFGL
LAPHQSLDHQRGGEQGAEAAAGLDDVVGGVRTAQAEEEGQVEQAEAGRERRDDQADAPAQQDVGNHGRHHQQAADAAGYAA
TCVEQAALKHQHVGEREDEDRQQLPRRRQEQRDQDVEDQVAPTADEQFRVDELEDLIFQFAGDQQDQYQADGQAVQVQ
EDALPLLLAQP*

>ORF29729 (SEQ ID NO:335)

TVPCRQLVLPGLQHPGRAVPAAVAAIAADLHPRAHRRADALRPVLRRWRTQRHRQAGGGGGHCQHPAARAHRPGHRCG
GQPRPALPDLLPQPEQSGRHQPLRPGRPRHPVLRRAAGDPGSGAAPGADRNRAGRRRDGRQPGGTQRIDPAAHAHRHP
RGR*

>ORF30221 (SEQ ID NO:337)

PSGHPPRQPGRPRPAQAGRRAGRQPRPPQPDADALHEAMAPESQPPSADAQGGAGWPDGATQLYQPQPRRRPARADLPRR
HFADRPAGAADEAGRSWPPDRRHP*

>ORF30736c (SEQ ID NO:339)

SHSFRSSCCGSAWRRRRECRTFSMTRFIRFDWSWMICVRRRSGASSSSDSCSSWAALIAPSGLRISWAMPNAVRRPRPAS
FICCACWAICEMSSRKISTCWSSSLRLIKLGCTVPGSGTTLVGGRLGFRHCFMCISIGLWRPRLAPCTSCLS
RAAWLARRMA*

>ORF30539 (SEQ ID NO:341)

DPQPAGRDPQRRPTAAGVRGTCGPPTPDADHPGPVEADEPGHRERPAALPSPPGRTAAARPEGVASAVRRRIPRQAAQR
QPTAPAAARCRRHDPHGPPTVEPGAEQPGAEERSSLQRPGLAERPAPGERPAGAGSHRRRSRTGGQTEQPVRT
LLYYRKQRHRPGPLSLPRTLREQPTDRLPQSRGRRLLPHLRPPAQTLTEAARMSRQKALIVDDEPDIRELLEITLG
RMKLDTRSARNVKEAASCWPASRSTCASPTCACRTAAASIWSSTSSAIHRPRWP*

>ORF31247c (SEQ ID NO:343)

FPAVRGYPVHRRRSGLFVGSCVRLPSAEFARVGEFDAEAAAFLIAIVVDPCVALAEEFAGEIEAQAGAFACSKEGFEO
VVQFVRRYAGTVVDDFQHRQVALRVAREAQPDLAAPVRLGAVAKTVLHQVAQHLVQLVWVHAGLDVAGTELQVQLAVVAQ
PAGVFVDEPLKPLLQVELLRFGLAATGELQDVLDQVHPLRLVLDLQRQASVRGIQFL*

>ORF30963c (SEQ ID NO:345)

LPAPAGRSPGRARGSARPGRARAPGRCSEDRSAPGCSAPGSTVGPGCGSGCRRHRAAGAVGCRCAACRGIRRTAEATPS
GRAAAVRPGGDGRAAGRSR*

>ORF31539c (SEQ ID NO:347)

GGCHQLPQATEVDRFGEVEVEGTGLERLDGQVAAVRGDHGRGLWMALLDVLDQIEAAAVRQAHVGEAQVERLAGQQLAA
SLTLRALRVSSFMMPRVISSSSISGSSTIRAFCRMLRAASVS*

>ORF31222 (SEQ ID NO:349)

TGYPRTAGNHSPRHEAGHPQRPQRQGSRELLAREPFDLCLDMRLPDGSGLDLVQYIQQRHPQTPVAMITAYGSLDTAIQ
ALKAGAFDFLTKPVDLGLRRELVATALRLRNPEAEEAPVDNRLLGESPPMRLRNQIGKLARSQAPVYISGESGSGKELV
ARLIHEQGPRIERPFVNVNGAIPSELMESEFGHKKGSFTGAIEDKQGLFQAAASGTLFLDEVADLPMAMQVKLLRAIQ
EKAVRAVGGQQEVAVARAHPRLRHPQGPQRRSRRRALPPGPLLPPQRHRAARTPLRERREDIPLLAERILKLAGDTGLPA
ARLTGDAQEKLKNYRFPGNVRELENMLERAYTLCEDDQIQPHDLRLADAPGASQEGAASLSEIDNLEDYLEDIERKLIMQ
ALEETRNWRTAAAQRLGLTFRSMRYRLKKLGID*

>ORF31266 (SEQ ID NO:351)

SWTPAAPATSRKPRVAGPRAVVPVRHAPAGRQPRSGPVHPAAPSTDPGGHDHRVRQPGHDPGAQGRCLRLPHQTGR
PRSLAGAGGNRPTLAQPGSRGSAGGQPPARRVAADARPAQPDHQAGAQPQAGLHQWVVRQRQGTGGAPDPRAGATYRAAV
RAGELRRDSLADGKRVLRPQERQLHWRYRRQAGPVPGRQRWHPVPRRSRRPADGHAGQTAPGDPGKGRARGRRPAGGRR
RTCASSAPPTRTSPPKSAPGASARTSTTASTSSCAYTAARTPRGHPAARRTHPQAPGRRHPRPAGRQADRRRTGEAEELP
LPGQPRAGKHAGARLYPVRPDPASRPPAPGRCAAGCOPGRRREPERNQPRGLPGRHRAQADHAGTRGDPLEPHRRGPA
PGPDVPLDALPPEKAGHRLKVRPVRQAFWFSSLRGDQPGRRGPGR*

>ORF31661c (SEQ ID NO:353)

TGAWLRASLPIWLRRARIGGDSPSRLSTGASSASGLRKRRAVATSSRKPRSTGLVRKSAPALSAWIAVSRLPYAVIM
ATGVCGWRCWMYWTRSRPLPSGRRMSVRHRSNGSRASNRLP*

>ORF32061c (SEQ ID NO:355)

RSWRKRPAPTSAAARSLWVAQRMRTCDGDLAAADRAHGLFLDRPEQFDLHGHQVGDFVEEQGATAGGLEQALLVFDAS
EAAFLVAEELAFHQLGGNRAAVHRHERPLDTWPLLVQARHQFLAAAGLATDVDRRLAARQLADLVAQGAHRRRLAEQAV
VHRRFLGFRVAQA*

>ORF32072c (SEQ ID NO:357)

GGSRGPSSARRLRRRGPCWRRGCARATATSCWPPTARTAFSWIARSSLTCMAIGRSATSSRNRPVPLAAWRPCLSS
IAPVLPFLWPKNLSISSEGIAPQFTGTNGRSIRGPCSWIRATSSLPLPDSPLM*

>ORF31784 (SEQ ID NO:359)

WKASSSATRKAASLALSCTSACRSPPAVAPCSSTSPTCRWPCRSNCGRSRKPCARAAASRRSPSHVRILCATHKDL
AAEVGAGRFRQDLYYRLNIELRVHRCANAARTSRCSPNASSAWPATPACRPPG*

>ORF32568c (SEQ ID NO:361)

GAKTKRPVFGQAFSLVDAQLFOAVAHRAERQAQALGRGGAVPAGLLECLHDQLALDVFQVVLEVVDFAQARGAFLAGTR
RIGQAQVVRDLVVFAQGIGALQHVFQLADVAREAVVLQLLCVAGQPGGRQAGVAGQALEDAFGEQRDVLAFAQRCTR
SSMTLRR*

>ORF33157c (SEQ ID NO:363)

TDGGARLVARRSGRRGDLAWRDPWRQGAAGGRRLEVVAAWPGTARGTGERSDDPQVRGGFPAAHGAGQGALRDS
AARRPHPDQHLLGTFLRQDADRRGAGKPQGVCGRTVAGTGGHAAGGPLGRVAPGLSRRHPLYRSGAWLRLALAERYRALP
QRAGPGTGVVPSAGGSHERAGTDHRPGPLRGWSPLRSENQKACLRTGLFTFSRCPAFSGGSASSGTSGPGAGPRRCGSS
GSPRVPA*

>ORF32530 (SEQ ID NO:365)

KGLSEDRPFGFRSSEATSRGVGGRVDDRFPPAHEIRQQTARRRCQDQPVAVVPGIQLQEPVEARHRTDIGDAFGRARAQPC
PVGHRLHVRQFRQQFCRRRPEAFQRLVGRRLVEARMFQGAADQDVAVAPRNRVAPLGQHARQEIRRALVEDHTFHRYH
GQFQAKRLQQLAAPGACRQQHLVATDLATRGRHADHSIAVAQPAHLRLFMQLEIGELLQGCPQ*

>ORF33705c (SEQ ID NO:367)

VIFLCSWQIGRSPVVSRDVVVVGAGVIGLLTARELALAGLRVTLVERGESGREASWAGGGIVSPLYPWRYSPAVTALAHW
SQDFYPALGQRLLDETGLDPEVHTVGLYWLDDQTEALQWARNHTRPLKEVPIEEAYAAVPGLAGFQRAVYMSGVANV
RNPRLARSLRASLQQFANLELHEQTEVRGWLDRGDRVVGVATSRGEIRGDKVLLAAGAWSGELLKPLGLELPVVPVKQGM
ILYKCAADFLPRMVLAKGRYAIPIRDRGHILIGSTLEHSGFDKPTDEAELRASAELLPELADMQPVAHWAGLRPGSP
EGIPIYIGPVGFDGLWLNTGHYRNGLVLAPASCRLLADLMSGREPIIDPAPYAPAGRL*

>ORF32832 (SEQ ID NO:369)

GFPAPRRSASCSPNPRCCRSRGCGRRAAESRSAPWPAPCAAGNPPRTCRGSSDLSPVPRAVPGQAASTRRSRLPPAA
PCRHGSRHARSPPRPLRRRATSRAPPSPVHATRDWRIVAGMPAMSAPGEDCAHWPRPTCRPPAGSLPARAPPRLPPRSA
LPSTAGCGCVPTAVPRSGRPGPASTGQRYGPRDRARSRRANAAPGPGRSATSAFGRSPGCSATDRAARRSRLPPRMPH
AHSRPAPPGSPAVRRAPAPGRSTGR*

>ORF33547c (SEQ ID NO:371)

GILGGRRDRLAALSVALQPGGDRPGALVAGLLPGPGAAFARRDRARSRGPYRWPVLAGPGRPDRGTAVGTOQPHPAVEGSA
DRGGGLRGGARAGRRLPAGGLHVGRGQCAQSSPGALIAGIPATIRQSRVA*

>ORF33205 (SEQ ID NO:373)

ARQARIAHIGHARHVDRPLEACAQPGHRRVGLLDRHFLQRPGVVACPLQCLGLVVQVQPVQANGMDLGIEPGLVEQTLQ
GRVEVLRPVRQGGHRRAVAPRIERRDDPASRPGCLPTLAPLHQGHQSGERQLPGQQADDASAYHYYISTHHRAPTD
PGTEKYHSKGSDADELPASTNSVESSPGEKPIIPAEVFIP*

>ORF33512 (SEQ ID NO:375)

SGETIPPPAQDASRPLSPRSTRVTRSPASASSRAVNRPMTPAPTTTSLTTGLLPIQEQRNITQRDQMLTNCLLQRTQ
SNLVPVKSPSYQPQRYSSHEIEWFEGGTIDSPIDPCDRDNCAHPPRQNEAGH*

>ORF33771 (SEQ ID NO:377)

KAHHTRRGIHPMKSSGLNLVELSIVLSILAI GTIALPTLPDRMKRDISRDIGDSLTHVMAARASSIQNGVII EVC GSG
DGSTCSEEWHLGWF SRNDRSQQILARHENTSRTDIHWRGFDKRLRYLPNGTSPTGNGRFFECKDDRIEWQLVLRQGRLR
VAGKSENKKLSYLC SRR*

>ORF34385c (SEQ ID NO:379)

WRAHCPCS RDSRS GEWDDWQTV CETVLSPPGAQV RELFIF ALSRHPEA ALPIEHQLPLDAIVLT FEETPVTCRAGAIQV
AQSLV EAPP MNIGATR IFMPGQYLLAPV VTAEP AEMPFLAAGTAVTATAH LDDH A VLYAAS PRSHM TSQAVTNITANVP
LHSVGE GGQRNCHAYRKDR*

>ORF33988 (SEQ ID NO:381)

SSRCAVAVTAVPAARNGISAGSAVTTGANRYWPGMKIRVAPIFIGGASTSDCATCLMAPALQVTGVSSNVRTIASSGNWC
SIGKAASGW RERAKISSLTCAPGGERTV SHTVCQSSHSPRLSLLQGQCALH*

>ORF34274 (SEQ ID NO:383)

KALLPVLQAVRELHFIPFASHPTLRSGLCYRDNALSTRQDYLALFLVEYCMRSICRSAGFSLIELMMVLVLVAIFASIA
VPSFNALIERNRIQTASEEYLQYARSEAVNRHANVSIRATQNNDWAKGLEIISGATTVQKHQGFQQV SLSASSATAE
LTFNATGTL SNQAANIDIKVCFAGDKSTGRLLTVQPSGRVILYPSSKQPDSCN*

>ORF34726c (SEQ ID NO:385)

RDLLETLVLLHGGRAADDQAFCPVIVLRRPAHIGMTV SFAASVLQAVEFLAGSLDSVALDQGVETGYGNAGEYGDQ
NQHHHQLDQKGAGAATNRAH AVLHKEKGQIILPSGERIVPVAETAGAESGMTKRYVKQFSHRLEHR*

>ORF34916 (SEQ ID NO:387)

GKPMSRETGF S MIEVLVALVLISIGV LGMVAMQGRTI QYTQESVQRNA AAM LASDLMEIMRADPDAVLNLRAQLREDSVY
YKAKGSDFP AAPARCA PLPADAKERL G CWAQQASKDLPGAS ALLNSQFYICRSPTPGTCDNTKGS AIEIQVAWRAMDGAC
FNASDSTLCTYSVRSEL*

>ORF35464c (SEQ ID NO:389)

RACLFSQFGADAVGAQGGVRGVETRSIHGSPGNLDFDGRAFGVVAGTRGWAATNVELAIQECGGSRQVFRGLLGPA AETF
LSICWQWRAARW GCGKVAALGLVVDRVFA*

>ORF35289 (SEQ ID NO:391)

IANSTFVAAQPRVPATTPKARPSKSR LPGE P WMERVSTPLTPPCAPTA SAPNCENKHALQNAER PIDGRTARGTRYKQL
PDPGDQPD LHRQQTQLSFPARPGRQPGK*

>ORF35410 (SEQ ID NO:393)

LHLVHLQRPLRIVRTSMLFSKMQKGLSMVELLVALAISSFLILGISQIYIDNKRNLYLQQGQAGNQENSRFVLMILLQQQL
 DKTAYRRLHDDNMENAFKSATFNGCRAFVAGETIAAATALKAGEYGVCLRYQPAYKGEHDCLGNEITGVPEKPFTNTPPV
 VVRLVYLPAGTLSCSRPDIAQSKSGELVSGLTDRLAEGVGPADRSERKVSSFVALQDVAGRPIRALRFSILAGSDNTS
 LRTGDDSQARDRWIVLYPESKSAIEADKGQIYQIARGNQTIRNLMP*

>ORF35907c (SEQ ID NO:395)

VDQANDDRGSICEGLFRNSGNFITEAIMLPVGGLIAQADTVLTRLGSCRSDSLASHKCTTAIECRGFESILHVVVVA
 TIGCLIQLLLQQHKNEAAIFLVAGLALLEKIVAFVVDVDLADPQDQEAAVSECHEQFYHR*

>ORF35534 (SEQ ID NO:397)

SWGSARSTSTTNATIFSSKARPATRKIAASFLLCCSNNWIROPIVAFTTTWRMLSNPRHSMAVVHLWLARLSLRQLPSR
 RVSTVSACAINPPTKGSMIASVMKLPFRKSPSILPLSSFAWSTYRAPVP*

>ORF35930 (SEQ ID NO:399)

VAVVPISPSRNRENWSVSVSQTSAWKRGSGQQIVANAKYPASSHYRMSPVVLSEHCASQSWQAATIQACQEMIARHAIAG
 SSFIPRAKAPSRSRQTKARFTK*

>ORF36246 (SEQ ID NO:401)

PNHQESHAMTLRHTSRQQGSTLLISLVILLMITLLAVSNMREVSLESRITGNLIEQKRLRNAGEAGLREGERRFFNTIKP
 PEVGSGCADCNSVKRPCILNLSALSVPRDDVHNNPVAALNGKTDNANSRVWMPYRGSDLNNPTQIDKDRAVTWQTITVPAG
 EQNNEAENPEYGNMMRGVGTYYETNSRALNKAGGETVLQAVHARLYTN*

>ORF26640c (SEQ ID NO:403)

GIQTRELALSVPFRAATGLLCSSRGTERALRFSMQGRLTLLSAHPLPTSGGLMVLKKRRSPSRSPASPALRRRFCSMR
 LPVIRLSSDTSRMLETARSVIINKTSEINNDPCCREWRRVMA*

>ORF36769 (SEQ ID NO:405)

CAGSARSTTKPTAAPSTRRAERLFYRPFMHACIPTDWSQRMHIQITRAGKSLLAAGCTLSILFASDSYATALNVSQQPL
 FLTQGVAPNLLFTLDDSGMSAWAYVPDGISGNSGRAGRSdynalYynPDYAYQVPKKLTLSDQIIVSDYVPVPTAAW
 QDGYAQGTTNLSSNNYRPQWGTGWLGCIDSSCNTGRAYYYTYKVSASCPAQPVSSNSCYTINALPTSQESNFIAWYSSY
 RNRILATKTAANLAFYSLPENVRLLTWGALNTSISGANSRSCQNNALLQFNQHKINFFNWLANSPASGGTPLHAALDRAG
 RFLQTNGTAYTTEDGKTYSCRASYHIMMDGIWNGRNVTGPNLDNQNQTFPDSTLYRQPQPYADSNASSLADLAFKYWT
 DLRPSIDNDLKPFMAYKSGDDSKDYWDPRNNPATWQHMVNFTVGLGLSYSLTLSNAPWTGSTFGNYEELMAGSKAWPSV
 DNDAAPGNVYDLWHAINSRGDFSAESPDSLQAFNKLTRISERNTSSSKPAMTSALQDDGTGDKLIRYSYQSSFASD
 KNWAGDLIRYKVESTSTGSKTQEWASAGALLDNRAPATRNIYIASNSGTNRLKPTWSNIEGSQLATWLNRPDKDNQAD
 TKGAQRVDIFRGQQNMDGFRQRQAVLGDIVHSSPAVVGPAQYLTYLANPIEPGSDYGTFKTEADQRSRPRVYVGSDGMH
 GFNIKTGVEEFAPIPTAVFEKLNLKTGISYQGGAHQYFVDAFPVSDAFFDGAWHTVLIGTLGAGGRGLFALDVTKPDDV
 KLLWEYDSSTDSDLGYTFSKPTVARLHSGQWAVVTGNGYSDNDKAALLLIDLKKGTLIKKLEVQSERGIANGLSTPRLA
 DNNSDGIADYAYAGDLOQNIWRFDLIGNTRNNDPDTNTSINPKPGDVDPSSAFRVSFSGAPLFRARADNNTRQPTAPPT
 LVRHPSRKGYIVIVGTGKYFEDDDAQADTSRAMTLYGIWDRQTKGESANSTPTIDRNALTAQMTTEANSTFGSVNRNIR
 LISQNPVKWYKDGTGTANSVDVASYGWRLNLEVNSKKGEMMIEDMFAAQVLLQLTPNDDPCDSGSTSWTYGLNPYT
 GGRTSFTVFDLKragIVDGSdyNGSVVSFAQDGLGGLAITQNEQRQSEACTGDECIIIFNPSDKSNGRQTWRVVEEK*

>ORF37932c (SEQ ID NO:407)

AGIAVGIRGLWPIEGAIRKGLVLLVEIAGGDVPTVPTVGHHDVIAGPAGICLSVFGGIISCAVGLQEASGSVKSRMQRST
 AAGRAVRQPIEEIDFVLLVELEQIVLAASAVGADATGVQGPPSETHVFRQAVKGQVGSGLCGQDAVAIVGVPYRKVAFL
 TGRKSIVGITVGAAHRLCRAASAYLISIVISSPGIAAAIDATKPAGSPLRAIVIAQVGGGALGVAILPGCCEAWHIVG
 NDDLIA*

>ORF38640c (SEQ ID NO:409)

LTSLNIAPCERLKAVGSAIAGDVNITGSGSSVQQCAGAPFLGFGRTGGSRLHLVTYKVARPVLVTGKAGLVAVADQLVA
GSVILQRGSHCWFGGGVALGNPCQDLIESLNQRVR*

>ORF39309c (SEQ ID NO:411)

SCLVIIASIAVAGNYCPLSAVQSGYGRFGEVTKVRVGTIAVFPKQLDIVRLGYIECEQAATSSTKRSQNSVPSSIEKG
IADDRCVSDEILVGTALVADAGKLVLFYCCRDESELFHAGFDVETMQHAIVGSNINSRAALVCLCLECAVVAAGFDGV
GQISEVLGRSDHGWRRVHDVP*

>ORF38768 (SEQ ID NO:413)

GTSCTRLQPWSDRPNTSLIWPTPSNPAATTAHSRQRQTSAALEFMLDPTMACCMVSTSKPAWKSSLSSLQQYSKSLTSLP
ASATRAVPTNISSTLHRSSAMPFSMELGTLF*

>ORF40047c (SEQ ID NO:415)

KHLAGSEHIFDHHFAFLAAIDLQIOPSPAIASHIRVRGTGCSVFVPLHRLANKPNIPVHATECGVRLCCHGLGCEGVAVD
GWGTVCAFALGLAIPDTIERHGSAGIGLSVIVLEVFSCTYDDVALTARMAYQGRRSRDGLTSIVVGASTEKGAAERYS
ESRRIYISGLEGIDRGICVWVVVAGIADQIEAPDISLQIASIGVVSNAIAVVISQARR*

>ORF40560c (SEQ ID NO:417)

PASPVVGHGWASDMSAHLRLLPDRQDEHPRPRPHSRTYSWHSRQRLGKPELELQELWREDVRGSCSFLLDDPPGLSSVTL
VAGVEDDALITSASLGLTLFVLNGQAT*

>ORF40238 (SEQ ID NO:419)

VAWPLPRTNSVNPRALVMSASSSTPATRVTDKPGGSSRNEHEPLTSSRHSSCSSSSGLPNLCLECHEVRECGRGRG
CSSCRRSGSSRWADISLAQPCPTTGLAGHILGTSGTDVFLRQTHQRPARNRVVLHYQAGPSRSRLRIGAATMKSNRGFTL
IELMIVVVVIIAILAGIAYPSYDEYVKRGNRTEGQALLSEAAATQERYFSQNNTYITTQADIGKLHMRNTSGTTVKSSTGK
YSLTVDTVANDGGYRLIANQAFNDLDCGNLTLTANGEKRTGSKKSVAECW*

>ORF40329 (SEQ ID NO:421)

RTTNLAGRRGEMNMNPLRLLATALAALALACPTFALSATNTFENVGVVEDVHPAAGLVVVDGQTYRLPNRVQQQDSPVIF
LVRQGQTVSFSGKLTSDLPEIESFYIIKQAPLVPFGSEQQQ*

Fig. 4-20

>ORF40709c (SEQ ID NO:423)

SLCSTSLLLLRSEGNERGLLDNVERLDFWQVAGEFAGERHCLSLTYQEYDRRVLLDTVGQAICLPIDYYQTGGRMNILD
HAHILERIRGTQGKGWASQS*

>ORF40507 (SEQ ID NO:425)

SMGRHIACPTVSNNRTRRSYSWYVRDRQCLSPANSPATCQKSSRSTLSSRPLSFPSDRSSNNEVEQRLHSHRVDDRRSNH
RYSWCWYRLPQLRRIREARESHRRTGITQRSSRYSRALFFTEQYLYHYPUSRHRQAAYAQHIGHHSEVLHRQIQPYRRYGSQ
RRRLSPYR*

>ORF41275c (SEQ ID NO:427)

VGGVGRAGTGGTGGEHYLLDAQGTAGQGFVIGIFAHKKPGLCRALPFSCLGALAPAFCNALLASSPAFLAVGGQGQVAT
IKIVECLVSDKAITSVVGYRIDGKAVFACGGLHCGARCVAHMQLADVGLGSDISIVL*

>ORF42234c (SEQ ID NO:429)

STSSRPEPSVAAPFPSGEGGSKVHSSNHRVAHETAMQIKLANPRGFAGVDRAlIEIVNRALDVFGPPIYVRHEVVHNKFV
VDNLRQRGAIFVEELDQVPDNVIVIFSAHGVSQAVRKEAEGRGLKVFATCPVTKVHMEVVRYSRDGHECVLIGHEGHP
EVEGTMQYDASNGGAIYLVEDEADVAALEVRKPEALHYVTQTTLSMDDTSKVIDALRAKFPQIQGPRKNDICYATQNQ
DAVKELADQCDMVLVVGSPNSSNSNRLRELAERMGTPAYLIDGAEDMQRGWFDGVRRIGITAGASAPEVLVRGVIAQLRE
WGASEEQELEGREENITFSMPKELRVKAL*

Fig. 4-21

>ORF41764c (SEQ ID NO:431)

RPPRGGRHHGPVRCQQRCHLPGGGRRRAGGAQARSPALRDPDHPVDGRHLEGHRCPARQVPADPGAAQERHLLCHPEPPGCREGTGRPVRHGPGGQPOQQFQLQPPARTRAHGHAGLPDRRRGHATRLVRRCA SHRNHRRRLRAGSAGARSDRP AT*

>ORF41284 (SEQ ID NO:433)

LGDHSAHQHFRGGACGDSATHTVEPAALHVLGAVDQVGRRHALGEFAQAVGVGTVGAHHQDHVALVGQFLHGLAV LGGIADVVLARPLDLRELGAQGIDDLRGVVHRQGGLGHVVQGFGLAHLQRGDVGLVLHQVDGTAVAGIVLAHGAFLGVAFMPDQHAFVAVA VAAVHHFHVHLGHQRAGRVENLQAAPLGFLADRLGNAGAEDDDVVRLHIEFLDEDGAALAQVHDEL VVHHLVTHDRAEDIEGTVDLDGAIHAGAEAAGIGEFDLHGLVGDAVIGRMNLATALPAWEGRSDRRFRPAGRR

>ORF41598 (SEQ ID NO:435)

PSRCRPSTGWSGSRSAGL RACAPPARRRPRPPPGRWHRCWHRTGPWCLPPRGGLHARSARIRGRRGCSAPLPCAPWSP AGRSRRKPSGRAPRLPCGPPGKRRGR*

>ORF42172c (SEQ ID NO:437)

QGSFVQSPRRPRDRHANQTRQSPRLLRRRGSRHDRQPCPRCLRPADL RASRGGAQQVRRGQPAPARRHLRRGTRSGAGQRHRHLQPRRRFPGGPQGSRGARPEGFRRDLPAGDQGAHSGALQPRPRMRADRA*

>ORF42233c (SEQ ID NO:152)

RRPAGLNRRSLRPSQAGRAVARFIRPITASPTRPPCKNSNPIAASAPAWIAPSRSSTVPSMSSARRSTCVTRWCTTSSSWTTCA SAAPSSSRNSIRCRTTSSSSAPTAFFRRSARKPRGAA*

Fig. 4-22

33A9 (SEQ ID NO:102)

CAAAGCATAAGACCAAGATGGCACATTGCCAACAAATACCCCTCCCCCTACCGTTGTTATCGTTGCCAGCCCT
 GATCTGGCGGAAAAGCCCGCTCCATGAATCGTATGGAGCCTCCATGTTCAACTCCTTCCTGGATATCCAGGAAGCC
 GTCCCCCACCACAAACAAAGCTGCCCCAGGGGATTCTACCTTCTCTGAGCAGCATGGAACCTGCTCGGCACGCC
 GCCGCCGGCAGCTACTGGAGAACATCTGGAGCGCCTCGCTATCCAAGCAGCAATTGAGGAGATCTACCGCGGCC
 CTGGCCAACATATGCCAGCTGGTCCAGCAGCTCCCTGCTCGAAAATCATCACCAGCCATCCAGGCGGATGATCG
 TCACGGCCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGAACCTACCTGCTCCGATCGGCGAGCGCCGGAGTC
 AGTCAGCCCAGGCTGAAGCCTGGTCGGCCGCCGGTATGGGCCCTGGCTCATGACATAGGCAAGATCGTCGAC
 CTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTGGAACGGACCGATCAACCAGCCATACCGCTCAAGTAC
 GAAGTCCCAGCAATACAGCTCCACGGCGTGCCTCAGCACTTCTCATCCACCAACTGCTACCGCGACTGCACTCGATT
 GGCTCAGTCGCTTCCAGAGCTGTTGCTCAATTGATCTACCTGTTGCTGGCAGTACGAGCACGCCGGATCCTCGC
 GAGATCATCGTAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGAATCCGGATCGAGCTCTGGCTGCACCGA
 GCAGTCGCTGCAGCGGAGCTGGCAGACGCCCTCGCTTCTGGTGAAGGACAAGTCAAGTGAATCAACCTAGCGGCC
 CGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAGCAAGCCTGCTGCCATCAACTGAGAGCCTACCTGCTG
 GCCCAGGGTATCGATGGGTGCCCTCCTCTAACGCCGTTCTCAGCATGCTCCAGGACCAAGCCGTATCCAGACAAA
 TGCCGAGGACAAGGCCATTGGACGGCACGGTAGACAACGGTCTGGATGGAGAAACAAGTTACGCTACTCAAGATTG
 CTCCAGCCTTGTCTGGACAGATGCTGCCAGCGCCCTCACCTACAGGGATCACTGGTCTGAAGATGGAACCGCC
 TCAACGGAAAAGCGGAAACGACCTGTGAAATTCCAACGGCCGGCTGAACAGCAGCAAGCACCAGAAACGAAGATGAT
 GCTCCATCAACCTGCCAGCGCTTGCACCGGAAACCGGCAAACGAGACGCAGGCGATTGCGAAACCCCTCAACTGATGATCAAG
 AAGAAACAGACGATTGTATGCACTTCTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACGACTCGCC
 GCTGCCTCCTACGAACACACGCCGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCTCC
 TGAAGCAATTGAAGATGTATTATGCTAGCAGAAGTACTGATCTGGACAGGGATTGCTGGTGGATGAAATCTGGCA
 TCGCGGCCGTCGCTTGTCAACGACACCAAGGCTTGGCATAACGTAGACGGACCGCCATGCTGGTACGCA
 GGAATTTCAGCGCTATGTCCAAGAGCATCCGGTCTGAAAAACTGGCCAAGCCAAGGAGACGACCCGGCTGGAAGCT
 GGTGCAGCGCGCTCGAAAAACAGGGCTTCTCGGAAGACCAAGTAAACCTGAACATCTGGACCATCAAGGTTCTG
 GTCCCTCGCAAGACGAAAGAGCTCAAGGCCACCTGCTCCAGGATCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAC
 CCAAGCCTACGGTACCGATGCCAGGGTGTGGAATGACGCCAGCAGCTCACCGAGGAGTACATCTTCGCG
 CACGATCTCCGGGAAGCCAGC

Fig. 5

33A9 SEQ ID NO:103

1 MNRHGASHVS TPFLDIQEAV PHPNNQSCP R GIHPSSEQHG TARHASPPAA
51 TGEHLAARLA IQAAIRGDL P AATGQLCGVG PAxPCFGKSS PCPSRRDDRS
101 RPGDRGYALK VRQTYLLPIG AAPESQSAQA EAWSAAAAYG ALAHDIGKIV
151 VDLQVELQDG STWHPWNGPI NQPYRFKYVK SREYQLHGAA SALFIHQLLP
201 RTALDWLSRF PELWAQLIYL FAGQYEHAGI LGEIIIVKADQ ASVAQELGGN
251 PDRALAAPKQ SLQRQLADGL RFLVKDKFKL NQPSGPSDGW LTQDALWLVS
301 KPAADQLRAY LLAQGIDGVP SSNAPFFSML QDQAVIQTNA EDKAIWTATV
351 DNGAGWRNKF TLLKIAPIALI WTDAAERPSP YSGSLVVEDG TASTEKPETT
401 CEIPNGPAEQ QQAPETKMLL HQPAPSVAKP ANETQAIAKP STDDQEETDD
451 LYALLGNINS PLEELDTSHD SPAASPTNTR GEENLQQPLG TKEPTDCAPE
501 AIEDVFMPSR STDLGQGFVG WMKSGIAARR LFINDTKALV HTVDGTAMLV
551 TPGIFKRYVQ EHPVLEKLAQ AKETTGWKLV QRAFEKQGLH RKTSKNLNIW
601 TIKVSGPRKT KELKAYLLQD PKLLFPEQPL DNPSLTVID AE*

Fig. 6A

33A9--ORF1 SEQ ID NO: 189

ATGGAGCCTCCATGTTCAACTCCTTCCTGGATATCCAGGAAGCCGTCCCCACCCAAACAACCAAAGCTGCCAGG
 GGGATTATCCTTCCTGAGCAGCATGGAACTGCTCGGCACGCCCTGCCGCCGGCAGCTACTGGAGAACATCTGGCAGC
 GCGCCTCGCTATCCAAGCAGCAATTGAGGAGATCTACCGCGGCCACTGGCAACTATGCCAGCTGGTCCAGCAGCTC
 CCTGCTTCGGAAAATCATCACCATGCCATCAGCGGGATGATCGATCACGCCCTGGAGATCGTGGCCTACGCACCTCA
 GGTACGGCAGACCTACCTGCTCCGATCGGCCAGCGCCGGAGTCACAGTCAGGCCAGGCTGAAGCCTGGTCCGGCCG
 CGCGTATGGCGCCCTGGCTATGACATAGGCAAGATCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGG
 CACCCCTGGAACGGACCGATCAACCAGCATACCGCTCAAGTACGTGAAGTCCCGCAATACCAGCTCCACGGCGTGC
 CTCAGCACTCTCATCCACCAACTGCTACCGCCACTGCACTCGATTGGCTCAGTCGCTTCCAGAGCTGTGGCTCAAT
 TGATCTACCTGTCGCTGGGAGTACGAGCACGCCGGATCCTCGCGAGATCATCGTGAAGGAGACCCAGGGCTCAGTT
 GCACAGGAGCTAGGAGGAATCCGGATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGCAGTTGGCAGACGGCCT
 TCGCTTCTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCCGCTGATGGATGGCTGACCCAGGACGCACCT
 GGCTGGTGAGCAAGCCTGCTGCCATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGTGCCCTCCTCTAAC
 GCGCCGTTCTCAGCATGCTCCAGGACCAAGCCGTATCAGACAAATGCCAGGACAAGGCCATTGGACGGCACGGT
 AGACAACGGTGTGGATGGAGAAACAAGTTCAAGCTACTCAAGATTGCTCCAGCCTGATCTGGACAGATGCTGCCGAGC
 GCCCCTCACCTACAGCGGATCACTGGTCGTGAAGATGGAACCGCCTCAACGGAAAAGCCGAAACGACCTGTGAAATT
 CCCAACGGCCGGCTGAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCCATCACCTGCCAGCGTTGCGAAACCC
 GGCAACAGAGACGCAGGGATTGCGAAACCTCAACTGATGATCAAGAAGAAACAGACGATTGTATGCACCTTGGTA
 ATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTGCCCTCCTACGAACACACGCCGGGAGGAG
 AACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCTCTGAAGCAATTGAAGATGTATTTATGCCCTAGCAG
 AAGTACTGATCTGGACAGGGATTGTTGGATGAAATCTGGCATCGCGCCCGTCGCCGTTCATCAACGACACCA
 AGGCTTGGTGCATACCGTAGACGGGACGCCATGCTGGTCACGCCAGGAATTTCAAGCGCTATGTCCAAGAGCATCCG
 GTGCTTGAAAACCTGGCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTCGAAAAACAGGGGCTTCA
 TCGGAAGACCACTGAAACATCTGGACCATCAAGGTTCTGGCTCTCGCAAGCAGAAAGAGCTCAAGGCCCTACC
 TGCTCCAGGATCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTATCACCGATGCCAGGA
 GGTGTGGAATGA

Fig. 6B

33A9--ORF2 SEQ ID NO:190

ATGTTTCAACTCCTTCCTGGATATCCAGGAAGCCGTCCCCACCCCAACAACCAAAGCTGCCCAAGGGGATTCATCCT
 TCCCTGAGCAGCATGGAACTGCTCGGCACGCCCTGCCGGCAGCTACTGGAGAACATCTGGCAGCGCCCTCGCTAT
 CCAAGCAGCAATTGAGGAGATCTACCGCGGCCACTGGCAACTATGCCAGCTGGTCCAGCAGCTCCCTGCTTGGAA
 AATCATCACCATGCCCATCCAGGCGGGATGATCGATCACGGCCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGAC
 CTACCTGCTCCGATCGCGCAGGCCGGAGTCACAGTCAGCCCAGGCTGAAGCTGGTGGCCGCCGCGTATGGCG
 CCCTGGCTCATGACATAGGCAAGATCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTGGAAAC
 GGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAGTCCCAGAATACAGCTCACGGCCTGCCTCAGCACTTCT
 CATCCACCAACTGCTACCGCGACTGCACTCGATTGGCTAGTCGCTTCCAGAGCTGTGGCTCAATTGATCTACCTGT
 TCGCTGGGAGTACGAGCACGCCGGATCCTCGCGAGATCATCGTGAAGGCAGACCAGGCTCAGTTGCACAGGAGCTA
 GGAGGCAATCCGGATCGAGCTGGCTGCACCGAAGCAGTCGCTGCAGCGGAGTTGGCAGACGGCCTCGCTTCTGGT
 GAAGGACAAGTTCAAGTGAATCACCTAGCGGCCGTCGTGATGGATGGCTGACCCAGGACGCACTCGGCTGGTGA
 AGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGTGCCCTCTAACGCCGTTCTC
 AGCATGCTCCAGGACCAAGCGTCATCCAGACAATGCCAGGACAAGGCCATTGGACGGCACGGTAGACAACGGTGC
 TGGATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCAGCCTGATCTGGACAGATGCTGCCGAGGCCCTCACCT
 ACAGCGGATCACTGGCGTTGAAGATGGAACCGCCTCAACGGAAAAGCGGAAACGACCTGTAATTCCAACGGCG
 GCTGAACAGCAGCAAGCACCAGAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCAAACCGGAAACGAGAC
 GCAGGCGATTGCGAAACCTCAACTGATGATCAAGAAGAACAGACGATTGTATGCACTTCTGGTAATATCAATTGCG
 CACTAGAAGAGCTAGACACTAGCCACGACTGCCGGCTGCCCTCCTACGAACACACGCCGGAGGAGAACCTACAGCAG
 CCACTAGGGACCAAGGAGCCAACAGATTGCGCTCTGAAGCAATTGAAGATGTATTATGCCCTAGCAGAAGTACTGATCT
 GGGACAGGGATTGCTGGTTGGATGAAATCTGGCATCGCCGCCGTCGCTGTTCATCAACGACACCAAGGCTTGGTGC
 ATACCGTAGACGGGACCGCCATGCTGGTCAGCCAGGAATTTCAGCGCTATGTCAGGACATCCGGTGGTGA
 CTGGCCCAAGCCAAGGAGACGCCGGCTGGAAGCTGGTGCAGCGCGCTGCAAACAGGGCTTATCGGAAGACCAG
 TAAAAACCTGAACATCTGGACCATCAAGGTTCTGGCTCTGCAAGACGAAAGAGCTCAAGGCTACCTGCTCCAGGATC
 CCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTCACTACCGATGCCAAGGAGGTGTGGAAATGA

Fig. 6C

ORF 3— 33A9 SEQ ID NO:191

ATGGAAC TGCTCGGCACGCCCTGCCGCCGGCAGCTACTGGAGAACATCTGGCAGCGCGCTCGCTATCCAAGCAGCAATT
 CGAGGAGATCTACCGCGGCCACTGGCAACTATGCCGAGCTGGTCCAGCAGCTCCCTGCTCGAAATCATCACCATG
 CCCATCCAGGCGGGATGATCGATCACGGCCTGGAGATCGTGGCCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCG
 ATCGGCGCAGCGCCGGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCCGGCCGCCGCGCGTATGGGCCCTGGCTCATGA
 CATAGGCAAGATCGTCGTGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTGGAACGGACCGATCAACC
 AGCCATACCGCTTCAAGTACGTGAAGTCCCGCAATACCAAGCTCACGGCGCTGCCCTCAGCACCTCTCATCCACCAACTG
 CTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTCCAGAGCTGTGGGCTCAATTGATCTACCTGTCGCTGGGAGCTA
 CGAGCACGCCGGGATCCTCGGCAGATCATCGTAAGGCAGACCAGGCCAGTTGCACAGGAGCTAGGAGGCAATCCGG
 ATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGGAGTTGGCAGACGCCCTCGCTCTTGGTAAGGACAAGTTC
 AAGTTGAATCAACCTAGCGGCCGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAAGCAAGCCTGCTGCCGA
 TCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGTGCCCTCCTAAGCGCCGTTCTCAGCATGCTCCAGG
 ACCAAGCCGTATCCAGACAAATGCCGAGGACAAGGCCATTGGACGCCACGGTAGACAACGGTCTGGATGGAGAAC
 AAGTTCACGCTACTCAAGATTGCTCCAGCCTGATCTGGACAGATGCTGCCGAGCGCCCTCACCCCTACAGCGGATCACT
 GGTCGTTGAAGATGGAACCGCCTCAACGGAAAAGCCGAAACGACCTGTGAATTCCCAACGGGCCGCTGAACAGCAGC
 AAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCCGAGCGTTGCCAAACGGCAAACGAGACGCCAGGCGATTGCG
 AAACCCCTCAACTGATGATCAAGAAGAACAGACGATTGTATGCACTTCTTGGTAATATCAATTGCCACTAGAAGAGCT
 AGACACTAGCCACGACTGCCGGCTGCCCTCCTACGAACACACGCCGGGAGGAGAACCTACAGCAGCCACTAGGGACCA
 AGGAGCCAACAGATTGGCTCCTGAAGCAATTGAAGATGTATTTATGCCCTAGCAGAAGTACTGATCTGGACAGGGATTG
 GTTGGTTGGATGAAATCTGGCATCGCGCCCGTGCCTGTCATCAACGACACCAAGGCTTGGTCATACCGTAGACCG
 GACCGCCATGCTGGTCAGCCAGGAATTTCAGCGCTATGTCCAAGAGCATCCGGTGCCTGAAAAACTGGCCAAGGCCA
 AGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGGTTGCAAAACAGGGCTCATCGGAAGACCAAGTAAAAACCTGAAAC
 ATCTGGACCATCAAGGTTCTGGCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCAAATTGCTGTT
 CCCTGAGCAGCCTCTGGACAACCCAAAGCCTACGGTCATCACCAGTGCAGGAGGTGGAATGA

Fig. 6D

ORF 4--33A9 SEQ ID NO:192

ATGATCGATCACGGCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCGATGGCGCAGGCC
 GGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCGGCCGCGCGTATGGCGCCTGGCTCATGACATAGGCAAGATCG
 TCGTCACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCTGGAACGGACCGATCAACCAGCCATACCGCTTC
 AAGTACGTGAAGTCCCGAATACAGCTCCACGGCCTGCCTCAGCAGCTTCTCATCCACCAACTGCTACCGCGACTGC
 ACTCGATTGGCTCAGTCGCTTCCAGAGCTGTTGCTCAATTGATCTACCTGTTGCTGGCAGTACGAGCACGCCGGA
 TCCTCGGCAGAGATCATCGTGAAGGCAGACCCAGGCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCT
 GCACCGAAGCAGTCGCTGCAGCGGAGTTGGCAGACGGCCTTCGCTTGGTAAGGACAAGTTCAAGTTGAATCAACC
 TAGCGGCCGCTGTGATGGTGAACCCAGGACGCACTCTGGCTGGTGAAGCAAGCCTGCTGCCGATCAACTGAGAGCCT
 ACCTGCTGGCCAGGGTATCGATGGGTGCCCTCTAACGCGCCGTTCTCAGCATGCTCCAGGACCAAGCCGTATC
 CAGACAAATGCCGAGGACAAGGCCATTGGACGGCCACGGTAGACAACGGTGCTGGATGGAGAAACAAGTTACGCTACT
 CAAGATTGCTCCAGCCTGATCTGGACAGATGCTGCCGAGCGCCCTCACCTACAGCGGATCACTGGTGTGAAGATG
 GAACCGCCTCAACGGAAAAGCGGAAACGACCTGTGAAATTCCAACGGGCCGGTGAACAGCAGCAAGCACCAGAACG
 AAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGAAACGAGACGCGAGCGATTGCGAAACCCCTCAACTGA
 TGATCAAGAAGAACAGACGATTGTATGCACTCTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACG
 ACTCGCCGGCTGCCTCTCACGAACACACCGGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCAACAGAT
 TGCCTCTGAAGCAATTGAAGATGTATTTATGCTTAGCAGAGTACTGATCTGGACAGGGATTGTTGGATGGAA
 ATCTGGCATCGCGGCCGTCGCTGTTCATCAACGACACCAAGGCTTGGTGCATACCGTAGACGGACGCCATGCTGG
 TCACGCCAGGAATTTCAGCGCTATGTCCAAGAGCATCCGGTCTGAAAAACTGCCAAGCCAAGGAGACGACCCGC
 TGGAGCTGGTGCAGCGCGCTCGAAAAACAGGGCTTCATCGGAAGACCAAGTAAAAACCTGAACATCTGGACCATCAA
 GGTTCTGGCCTCGCAAGACGAAAGAGCTAAGGCTACCTGCTCAGGATCCAAATTGCTGTCCCTGAGCAGCCTC
 TGGACAACCAAGCCTACGGTACCGATGCCGAAGGAGGTGTTGAATGA

Fig. 6E

ORF5--33A9 SEQ ID NO:193

ATGCTCCAGGACCAAGCCGTATCCAGACAATGCCGAGGACAAGGCCATTGGACGGCACGGTAGACAACGGTGTGG
 ATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCCAGCCTGATCTGGACAGATGCTGCCAGCGCCCTCACCTACA
 GCGGATCACTGGCGTTGAAGATGGAACCGCCTCAACGGAAAAGCGGAAACGACCTGTGAAATTCCAACGGCCGGCT
 GAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCATCAACCTGCCGAGCGTTGCGAAACCGGAAACGAGACGCA
 GCGATTGCGAAACCCCTCAACTGATGATCAAGAAGAAACAGACGATTGTATGCACTCTGGTAATATCAATTGCCAC
 TAGAAGAGCTAGACACTAGCCACGACTGCCGGCTGCCCTCCTACGAACACACCGGGGAGGAGAACCTACAGCAGCCA
 CTAGGGACAAGGAGCCAACAGATTGCGCTCTGAAGCAATTGAAGATGTATTTATGCTTAGCAGAGTACTGATCTGGG
 ACAGGGATTGTTGGATGAAATCTGGCATCGCGCCGTCGCTGTTCATCAACGACACCAAGGCTTGGTGCATA
 CCGTAGACGGGACCGCCATGCTGGTACGCCAGGAATTTCAGCGCTATGTCCAAGAGCATCCGGTCTGAAAAACTG
 GCCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTCGAAAAACAGGGCTTCATCGGAAGACCAAGTAA
 AACCTGAACATCTGGACCATCAAGGTTCTGGCCTCGCAAGACGAAAGAGCTAAGGCTACCTGCTCCAGGATCCCA
 AATTGCTGTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTACCGATGCCGAAGGAGGTGTTGAATGA

Fig. 6F

ORF6--33A9 SEQ ID NO:194

ATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGAAACGAGACGCAGGCATTGCGAAACCCCTCAACTGATGA
TCAAGAAGAACAGACGATTGTATGCACTCTTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACGACT
CGCCGGCTGCCCTCTCCTACGAACACACGCGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGC
GCTCCTGAAGCAATTGAAGATGTATTATGCCCTAGCAGAAGTACTGATCTGGACAGGGATTGTTGGATGAAATC
TGGCATCGCGGCCGTCGCTGTTCATCAACGACACCAAGGTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCA
CGCCAGGAATTTCAAGCGCTATGTCCAAGAGCATCCGGTGTGTTGAAAAACTGGCCAAGGAGACGACCGGCTGG
AAGCTGGTGCAGCGCGTGTGAAACAGGGCTTCATCGGAAGACAGTAAACACTGAACATCTGGACCATCAAGGT
TTCTGGTCCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTG
ACAACCCAAGCCTACGGTCATCACCGATGCCGAAGGAGGTGGAATGA

Fig. 6G

ORF7--33A9 SEQ ID NO:195

ATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGAAACGAGACGCAGGCATTGCGAAACCCCTCAACTGATGATCA
AGAAGAACAGACGATTGTATGCACTCTTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACGACTCGC
CGGCTGCCCTCTCCTACGAACACACGCGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCT
CCTGAAGCAATTGAAGATGTATTATGCCCTAGCAGAAGTACTGATCTGGACAGGGATTGTTGGATGAAATCTGG
CATCGCGGCCGTCGCTGTTCATCAACGACACCAAGGCTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTACGC
CAGGAATTTCAAGCGCTATGTCCAAGAGCATCCGGTGTGTTGAAAAACTGGCCAAGGAGACGACCGGCTGGAAG
CTGGTGCAGCGCGTGTGAAACAGGGCTTCATCGGAAGACAGTAAACACTGAACATCTGGACCATCAAGGTTTC
TGGTCCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTG
ACCCAAGCCTACGGTCATCACCGATGCCGAAGGAGGTGGAATGA

Fig. 6H

ORF8--33A9 SEQ ID NO:196

ATGCCTAGCAGAAGTACTGATCTGGACAGGGATTGTTGGATGAAATCTGGCATCGCGCCGTCGCTGTTCAT
CAACGACACCAAGGCTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCAGGCCAGGAATTTCAAGCGCTATGTCC
AAGAGCATCCGGTGTGTTGAAAAACTGGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGTGTGAAAAAA
CAGGGGCTTCATCGGAAGACAGTAAACACTGAACATCTGGACCATCAAGGTTCTGGTCCCTCGCAAGACGAAAGAGCT
CAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAAGCCTACGGTCATCACCG
ATGCCGAAGGAGGTGGAATGA

Fig. 6I

ORF9--33A9 SEQ ID NO:197

ATGAAATCTGGCATCGCGCCCGTCGCCTGTTCATCAACGACACCAAGGCTTGGTCATACCGTAGACGGGACGCCAT
GCTGGTCAGGCCAGGAATTTCAAGCGCTATGTCCAAGAGCATCCGGTCTGAAAAACTGGCCAAGCCAAGGAGACGA
CCGGCTGGAAGCTGGTGCAGCGCGCTCAGAAAACAGGGGCTTCATCGGAAGACCAGTAAAACCTGAACATCTGGACC
ATCAAGGTTCTGGTCTCGCAAGACGAAAGAGCTAAGGCCTACCTGCTCCAGGATCCAAATTGCTGTTCCCTGAGCA
GCCTCTGGACAACCAAGCCTACGGTCATCACCGATGCCAGGAGGTGTGGAATGA

Fig. 6J

ORF10-33A9 SEQ ID NO:198

ATGCTGGTCAGGCCAGGAATTTCAAGCGCTATGTCCAAGAGCATCCGGTCTGAAAAACTGGCCAAGCCAAGGAGAC
GACCGGCTGGAAGCTGGTGCAGCGCGCTCAGAAAACAGGGGCTTCATCGGAAGACCAGTAAAACCTGAACATCTGGACC
CCATCAAGGTTCTGGTCTCGCAAGACGAAAGAGCTAAGGCCTACCTGCTCCAGGATCCAAATTGCTGTTCCCTGAG
CAGCCTCTGGACAACCAAGCCTACGGTCATCACCGATGCCAGGAGGTGTGGAATGA

Fig. 6K

ORF 1--33A9 SEQ ID NO:199

MEPPMFQLLSWISRKPSPTTAKAPGGFILPLSSMELLGTPRRQLLENIWQRASLSKQQFEEIYRRPLANYAELVQQL
PASENHHAHPGGMDIHGLEIVAYALKVROTYLLPIGAAPESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGSTW
HPWNGPINQPYRFKVKREYQLHGAASALLIHQLPRTALDWLSRFPELWAQLIYLFAQYEHAGILGEIIVKADQASV
AQELGGNPDRALAAPKQSLQRQLADGLRFLVKDKFKLNQPSGPSDGWLTDALWLSKPAADQLRAYLLAQGIDGVPS
APFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAEERPSPYSGSLVVEDGTASTEKPETTCEI
PNGPAEQQQAPETKMMHLQPAVAKPANEQIAKPSSTDQEEETDDLYALLGNINSPLEELTSHDSPAASPTNTRGE
NLQQPLGTKEPTDCAPEAIEDVFMPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHP
VLEKLAQAKETTGWLKVQRAFEKQGLHRKTSKNLNIWTKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLT
GVE.

Fig. 6L

ORF2--33A9 SEQ ID NO:200

MFQLLSWISRKPSPTTAKAPGGFILPLSSMELLGTPRRQLLENIWQRASLSKQQFEEIYRRPLANYAELVQQLPASE
NHHHAHPGGMDIHGLEIVAYALKVROTYLLPIGAAPESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGSTWHPWN
GPINQPYRFKVKREYQLHGAASALLIHQLPRTALDWLSRFPELWAQLIYLFAQYEHAGILGEIIVKADQASV
AQELGGNPDRALAAPKQSLQRQLADGLRFLVKDKFKLNQPSGPSDGWLTDALWLSKPAADQLRAYLLAQGIDGVPS
SMLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAEERPSPYSGSLVVEDGTASTEKPETTCEI
PQNGPAEQQQAPETKMMHLQPAVAKPANEQIAKPSSTDQEEETDDLYALLGNINSPLEELTSHDSPAASPTNTRGE
NLQQPLGTKEPTDCAPEAIEDVFMPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHP
VLEKLAQAKETTGWLKVQRAFEKQGLHRKTSKNLNIWTKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLT
VITDAEGGVE.

Fig. 6M

ORF2-33A9 SEQ ID NO:201

MELLGTPRRQQLLENIWQRASLSKQQFEEIYRRPLANYAELVQQLPASENHHAHPGGMIDHGLEIVAYALKVRQTYLLP
IGAAPESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGSTWPNGPINQPYRFKVVKSREYQLHGAASALLIHLQ
LPRTALDWLSRFPELWAQLIYLFAQQYEHAGILGEIIVKADQASVAQELGGNPDRALAAPKQLQRQLADGLRFLVKDKF
KLNQPSGPSPDGWLTDQDALWLSKPAADQLRAYLLAQGIDGVPSSNAPFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRN
KFTLLKIAPALIWTDAEERPSPYSGSLVVEDGTASTEKPETTCEIPNGPAEQQQAPETKMMILHQPAPSVAKPLANETQAI
KPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTDCAPEAIEDVFMPSRSTDLGQGF
VGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTGWLKVQRAFEKQGLHRKTSKNLN
IWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSSLTVITDAEGGVE.

Fig. 6N

ORF4-33A9 SEQ ID NO:202

MIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAYGALAHIDGKIVVDLQVELQDGSTWHPWNGPINQPYRF
KYVKSREYQLHGAASALLIHQLLPTALDWLSRFPELWAQLIYLFAQQYEHAGILGEIIVKADQASVAQELGGNPDRALA
APKQLSLQRQLADGLRFLVKDKFKLNQPSGPGWLTQDALWLVSCKPAADQLRAYLLAQGIDGVPSSNAPFFSMLQDQAVI
QTNAEDKAIWTATVDNGAGWRNKFLLKIAPIALIWTDAERPSYSGSLVVEDGTASTEKPETTCEIPNGPAEQQQAPET
KMMLHQPAKSVAKPANEQIAKPSDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTD
CAPEAIEDVFMPRSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTG
WKLVQRAFEKQGLHRKTSKLNLIWTIKVSGPRKTKELKAYLLQDPKLLFPEOPLDNPSLTIVITDAEGGV.

Fig. 60

ORF5--33A9 SEQ ID NO:203

MLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSGPSLVEDGTASTEKPETTCIEIPNGPA
EQQQAPETKMMHLHQPAPSVAKPANEQTQAIAKPSTDDQEETDDLYALLGNINSPLEELDTSHSPAASPTNTRGEENLQQP
LGTKEPTDCAPEAIEDVFMPRSSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKL
AOAKETTGWKLVORAPEKOGHLRKTSKLNLIWTIKVSGPRKTKEALKAYLLODPKLLFPEQPLDNPSSLTVITDAEGGV.

Fig. 6P

ORF6-33A9 SEQ ID NO:204

MMLHQPAPSVAKPANETQAIAKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTDC
APEAIEDVFMPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTGW
KLVQRAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSSLTVITDAEGGVE.

Fig. 6Q

ORF7-33A9 SEQ ID NO:205

MLHQPAPSVAKPANETQAIAKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTDCA
PEAIEDVFMPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTGW
KLVQRAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSSLTVITDAEGGVE.

Fig. 6R

ORF8--33A9 SEQ ID NO:206

MPSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTGWKLVQRAFEK
QGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSSLTVITDAEGGVE.

Fig. 6S

ORF9--33A9 SEQ ID NO:207

MKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHPVLEKLAQAKETTGWKLVQRAFEKQGLHRKTSKNLNIWT
IKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSSLTVITDAEGGVE.

Fig. 6T

ORF10--33A9 SEQ ID NO:208

MLVTPGIFKRYVQEHPVLEKLAQAKETTGWKLVQRAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPE
QPLDNPSSLTVITDAEGGVE.

Fig. 6U

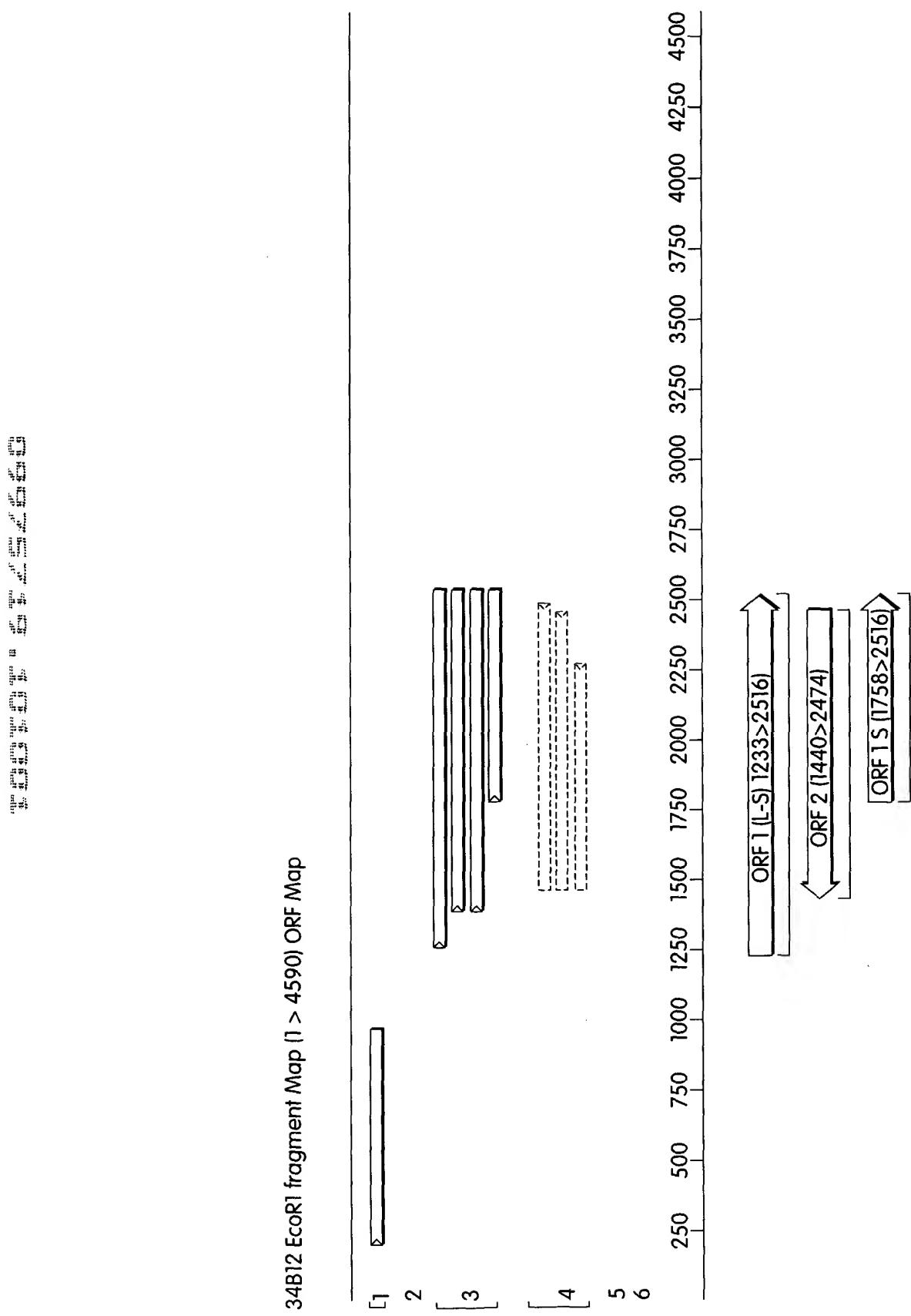


Fig. 7A

Sequence: 34B12 EcoR1 fragment From: 1 To: 4590

10	20	30	40	50	60
GAATTCCATG	GCGCCGTGGA	GGAGGCTTCC	GAGTCGCCGG	TGGCAGGCGT	ACGGGCCGGC 60
AACTACCAGG	TCGACCTGGA	CGATGCGAGC	TTTGCCCGCC	AGGTAGAACG	CCTGCAGGCC 120
CACGTGAGGG	CCGGCGACGT	GTTCCAGATC	GTACCTTCGC	GCAGCTTCAG	CATGCCGTGC 180
GCGGACCCCT	GGCGGGCCTA	TCGCCAGTTG	TGCCTGCGCA	ACCCCAGCCC	GTACCGCTTC 240
TTCCTCGATG	CGGGGGACTT	CTGCCTGTTC	GGCGCTTCGC	CGGAGTCGGC	ATTGAAGTAC 300
310	320	330	340	350	360
GACGCGGAGA	GTCGCGAGGT	GGAACTCTAT	CCCATTGCCG	GCACCCGCC	GCGCGGATGC 360
GATGCCCGGG	GCGCCATCGA	TGCGGAACTG	GACAATGCC	TGGAAGCGGA	GTTGCCTG 420
GATGCCAAGG	AGATGCCGA	GCACATGATG	CTGGTCGACC	TGGCGCGCAA	CGATCTGGCG 480
CGCGTCTGCC	GCAGCGGTAC	CCGGCAGGTG	CGCGACATGC	TCAAGGTCGA	TCGCTACAGC 540
CACGTGATGC	ACCTGGTCTC	GCACGTGGCT	GGCGAAGTGC	ACGGCGAACT	GGATGCCGTG 600
610	620	630	640	650	660
CATGCCCTACC	GTGCCTGCCT	GAACATGGGC	ACCCCTGGTCG	GCACGCCGAA	GGTCCGTGCC 660
ATGCAGTTGC	TGCGGCAGTA	CGAGGATGGC	TATCGCGGCA	GCTACGGTGG	TGCGATCGGC 720
ATTCTCGACA	GCGCCGGCAA	CCTCGATACC	AGCATTGTCA	TCCGCTCCGC	CGAGGTCCGC 780
GAAGGTATCG	CGCGGGTTCG	GGCAGGCGCC	GGCGTGGTGC	TGGATTCGGA	TCCACGGCTG 840
GAGGCCGAGG	AAACCCGCAA	CAAGGCGCTG	GGCGTGTGA	CCGCCGTGGC	CGCTGCCGAA 900
910	920	930	940	950	960
CGCGAAAGGG	GAGAGCGCGA	TGCGCATCAC	GCTGTTGGAT	AACTTCGATT	CCTTCACCTA 960
CAACCTGGTC	GAGCAGTTCT	GCCTGCTCGG	CGCGGAGGTC	CGGGTGTGC	GCAACGATAC 1020
GCCGTTGCCG	ACGATCCAGG	CGGCATTGCT	GGCGACGGT	TGCGAACTGC	TGGTGCTGTC 1080
GCCGGGGCCC	GGTCGGCCGG	AAGACGCCGG	CTGTATGCTG	GAATTGCTCG	CCTGGGGCCG 1140
CGGGCGCTTG	CCGGTGCTCG	GGGTCTGCCT	CGGCCACCCAG	GCGCTGGCGC	TGGCCGCCGG 1200
1210	1220	1230	1240	1250	1260
TGGCGCGGTG	GGCGAGGCGA	GGAGGCCGCT	GCATGGCAAG	AGCACGTCCC	TGCGTTTCGA 1260
TCAGCGTCAC	CCGCTGTTCG	ACGGCATCGC	TGACCTGCC	GTGGCGCGCT	ACCACTCGCT 1320
GGTGGTCAGT	CGCCTGCCGG	AAGGTTTCGA	CTGCCTGGCC	GATGCCGATG	GCGAGATCAT 1380
GGCGATGGCC	GATCCGCGCA	ATCGACAGCT	GGGCTTGCAA	TTCCATCCCG	AGTCGATTCT 1440
CACCACCCAC	GGCCAGCGTC	TGCTGGAGAA	CGCTCTACTC	TGGTGCGGCG	CGTTGGCGGT 1500

Fig. 7B

Sequence: 34B12 EcoR1 fragment From: 1 To: 4590

1510	1520	1530	1540	1550	1560	
CGCGGAGCGC	CTTCGGGCCT	GAGCAGCGCT	GCGCAGTTTC	GACCGAGGCT	CGGTTGCCAG	1560
GCCGGCGCAT	CGTCGAAACG	CTGGCGGCC	AGTCGCGCA	GGCGCTGGCG	GGCGCTTCG	1620
AGAAAGCGAC	GGAAGCTGCG	CTCGGATTCC	AGCGCGGTGT	TGTAGTAGCA	ATACACCTG	1680
GTGTCGATGC	CGCCCGGTT	GTACAGTTCG	CTGAGGACTG	CCAGGGTACC	GTTGCGCAGG	1740
CGTTCCCTCGA	CGAAATAATG	CGGCGAGATG	CCCCATCCGA	CGCCGGCTTC	CACCAAGACGC	1800
1810	1820	1830	1840	1850	1860	
AGCATGTCGT	CGAACGTTTC	CACGAAGAGC	ACCTTGTGCG	TGACCGGCCG	CAGCAGGTT	1860
GAATGCTGCC	CGGAGCGGCT	GCCGAGGCTG	ATCTGCCGGT	AATTGGCCAG	GCTCGCGATG	1920
CTGTGCAGGG	AGGCATTGCA	CAACGGGTGC	TGCGGATGGG	CGACGACGAA	CGCCTTGGTG	1980
TAGCCGAGCA	CGCACTGGTT	GAAGCGGGAG	ATCTTCAGTT	CCTCGTCGAT	GGTGATGGCG	2040
ATATCGATTT	CCGCCTTGTC	CTGCTGATC	GTCGCCAGGC	TATCGCGGG	CGAGGTGCGT	2100
2110	2120	2130	2140	2150	2160	
ATCAGGGCTGA	CCATGTTGAA	ATCGTCGAGC	AGTACGCTGC	TCACCGTATC	GCAGAACGAC	2160
GGCGGGATGG	CGGTGTCCAG	CAGCACCCGG	AGATTGCGCG	GACCCCTTGT	GAGATTGAAG	2220
GCGATGTCGC	CGATCAGCTG	CTGGTAGTTC	AGCAGGCTGC	GCATGTAAGG	GATCAGCGA	2280
AGCGCCTGCT	CGGTGGGTT	GACCTTGTAG	CCGTCCCGAC	GGACCAGCTC	CACGCACAGG	2340
TCGATTTCCA	GGTTGCTGAC	CGCCGAGCTG	ACCGCGGTGT	GCGACTTGC	CAGGATCCGC	2400
2410	2420	2430	2440	2450	2460	
GCAGCGGAGG	AAATCGAAC	GGAGGGCGATG	ACCTGGAGGA	ACATGTTCAC	GTGATTCAAG	2460
TTATGAATAG	GCATCCCTTA	TTCCTTTAT	TGGGTGGCGC	GTGCCGCTTC	CCTTGATCGG	2520
GTCAGGTGTC	CGCTACTGTG	GAAGAACGCT	CGAGGACTCG	ATAGATAGCG	CCCGAGTGT	2580
TCAACTTGTG	TTCTGGATGA	CGTTTCATC	GGGGAAACCT	CCCGTCGGTC	AGTGAATCGC	2640
AAGGGCTGGC	GTGCGAGGGT	GGAATCGGCC	GCCGGCTCGC	TTCTGCGCG	GCAGGGCGCAC	2700
2710	2720	2730	2740	2750	2760	
GGCACGGGGA	GTCGTCGTT	TGGAGGTGAG	GGATGACGGC	TCTGTTTCAG	GATATTGTTA	2760
TAATTATGTG	AAAGAACGAC	TTATTCAAC	GAAATATGTT	TCATATTGCT	CGTTAAATTC	2820
GACGAAAAGA	AAATCCGGAT	ATTTACCGGT	TATTAACGC	TAATACCAAG	TGCCTAATAC	2880
CAAAGTATTA	ACGCTGGTAT	GCCGGCATGT	CGTGGTCGGT	CGTGGAGCGA	GCCGAGCTAG	2940
GGACGGTTCT	AATAAACCAA	AAAATTATGT	CGCGTACGTC	TAACGACCAGA	AACCTATGTC	3000

Fig. 7C

Sequence: 34B12 EcoR1 fragment From: 1 To: 4590

3010	3020	3030	3040	3050	3060
TCTTGTAGC GTAGCCACCG GCCAGGCCGG TACGGACCCG GGATGGCCCT GGCGCGACCT 3060					
ATGCGGTAG AATCCGCGGC CTTGCAGCG GATAACCGAG CTTCGCTCGA AGGTGTGCG 3120					
GTGCCGTGCC GTGGAATCGG CCGCCGGCTC GCTTTCTGCG CGGCGGGCGC ACGGCGACGG 3180					
GGAGTCGTCG TTTGGAGGT GAGGGATGAC GGCTCTGTT CAGGATATT TTATAATTAT 3240					
GTGAAAGAAG AGCTTATTTC AACGAAATAT GTTTCATATT GCTCGTAAAT TCGACGAAAA 3300					
3310	3320	3330	3340	3350	3360
GAAAATCCGG ATATTTACCG GTTATTAAAC GTTAATACCA AGGGCCTAAT ACCAAAGTAT 3360					
TAACGCTGGC ATGCCGGCAT GTCGTGTTCG GTCGTGGAGC GAGCCGAGCC AGGAACGGTT 3420					
CTAAGAACG AAAAAATTAT GTCGCGTAGG TCTAACGACC GAAACCTATG TCTTTGTTA 3480					
GCGTAGCCAC CGGCCAGGCC GGTACGGATG CCAGGGATGGC CCTGGCGCGA CCTATGCGGT 3540					
TAGAATCCGC GGCCTTGCAG GCGGATCCCC GGGGTTTGCT CAAGGGGACA CGGGTGCCGT 3600					
3610	3620	3630	3640	3650	3660
GCCCGAAACC TGCAATCGTC AGTTCCCTGC GGTCCAGCCT GCCGCCGGGT ATAAAATCGA 3660					
GAGACCGCCT GTTGCCTT CAGGTGTAGC GACTATGACG CACATTCCG AACGACTCCT 3720					
GGTACAGGCC CACCTGGCCG CCAAGCAACC CCGTGTGTG AGCGAGCAGG AGAGCGCCGA 3780					
GCATCGCGCG GCGATCGCGG CCGAAGTGA GGCAGCAAAT GCTGTACTGG TGGCGCATT 3840					
CTACTGCGAC CCGGTGATCC AGGCCTTGGC CGAGGAGACC GGCGGTTGCG TATCCGATTC 3900					
3910	3920	3930	3940	3950	3960
GCTGGAGATG GCCCGTTTCG GCAACCAGCA TCCGGCGCAG ACGGTGGTCG TGGCCGGGGT 3960					
GCGCTTCATG GGGGAGACGG CGAAGATCCT CAACCCCTGAG AAGCGTGTGC TGATGCCGAC 4020					
CCTCGAAGCG ACCTGCTCGC TCGACCTGGG ATGCCCGGTG GATGAATTCT CGGCTTCTG 4080					
CGACCAGCAC CCGGAACCGGA CCGTGGTGGT CTATGCGAAC ACCTCCGCGG CGGTGAAGGC 4140					
ACGCGCCGAC TGGGTGCGTA CCTCCAGTTG CGCGGTGGAG ATCGTCGAAC ACCTGATGGA 4200					
4210	4220	4230	4240	4250	4260
CAACGGCGAG CCCATCCTCT GGGCGCCGGA CCAGCACCTG GGACGCTACA TCCAGCGCGA 4260					
GACGGGGGCC GACATGCTGC TCTGGGATGG CGCCTGTATC GTCCACGAGG AGTTCAAGGC 4320					
CAAGCAGCTG GAAGACATGA AGGCCTCTA CCCGGACGCC GCCATCCTGG TCCACCCGA 4380					
ATCGCCGGAA AGCGTGGTCG CGCTGGCCGA TGCCGTGGGC TCGACCGAGCC AGTTGATCAA 4440					
GGCCGCGCAG ACCCTGCCGA ACAAGACCTT CATCGTCGCC ACCGATCGCG GCATCTCTA 4500					

Fig. 7D

90/133

Sequence: 34B12 EcoR1 fragment From: 1 To: 4590

4510 4520 4530 4540 4550 4560
CAAGATGCAG CAGTTGTGCC CGGACAAGGA TTTCATCGAG GCCCCCACCG CCGGCAACGG 4560
CGCCGCCCTGC CGCAGTGCGC GCACGTCCCCG 4590

Fig. 7E

91/133

Sequence: 34B12 ORF 1 L-S From: 1 To: 1284

10 20 30 40 50 60
ATGGCAAGAG CACGTCCCTG CGTTTCGATC AGCGTCACCC GCTGTTCGAC GGCATCGCTG 60
ACCTGCGCGT CGCGCGCTAC CACTCGCTGG TGGTCAGTCG CCTGCCGAA GGTTTCGACT 120
GCCTGGCCGA TGCCGATGGC GAGATCATGG CGATGGCCGA TCCGCGCAAT CGACAGCTGG 180
GCTTGCAATT CCATCCCGAG TCGATTCTCA CCACCCCACGG CCAGCGTCTG CTGGAGAACG 240
CTCTACTCTG GTGCGGCGCG TTGGCGGTGCG CGGAGCGCCT TCAGGGCCTGA CGGGCGCTGC 300
310 320 330 340 350 360
GCAGTTTCGA CCGAGGCTCG GTTGCGAGGC CGGCGCATCG TCGAAAACGCT GGCAGGCCAG 360
TTCGCGCAGG CGCTGGCGGG CGCTTTCGAG AAAGCGACGG AAGCTGCGCT CGGATTCCAG 420
CGCGGTGTTG TAGTAGCAAT ACACCTTGGT GTCGATGCCG CCCGGTTCGT ACAGTTCGCT 480
GAGGACTGCC AGGGTACCGT TGCGCAGGCG TTCCTCGACG AAATAATGCG GCGAGATGCC 540
CCATCCGACG CCGGCTTCCA CCAGACGCAG CATGTCGTCG AAGTTTCCA CGAAGAGCAC 600
610 620 630 640 650 660
CTTGTGCGCTG ACCGGCCGCA GCAGGTTCGA ATGCTGCCCG GAGCGGCTGC CGAGGCTGAT 660
CTGCCGGTAA TTGGCCAGGC TCGCGATGCT GTGCAGGGAG GCATTGCACA ACGGGTGCTG 720
CGGATGGGCG ACGACGAACG CCTTGGTGTGTA GCCGAGCACG CACTGGTTGA AGCGGGAGAT 780
CTTCAGTTCC TCGTCGATGG TGATGGCGAT ATCGATTTCG GCGTTGTCCT GCTTGATCGT 840
CGCCAGGCTA TCGGCGGGCG AGGTGCGTAT CAGGCTGACCG ATGTTGAAAT CGTCGAGCAG 900
910 920 930 940 950 960
TACGCTGCTC ACCGTATCGC AGAACGACGG CGGGATGGCG GTGTCCAGCA GCACCCGGAG 960
ATTGCGCGGA CCCCTGTTGA GATTGAAGGC GATGTCGCG ATCAGCTGCT GGTAGTTCA 1020
CAGGCTGCGC ATGTAAGGGTA TCAGGCGAAG CGCCTGCTCG GTGGGGTTCGA CCTTGTAGCC 1080
GTCCCGACGG ACCAGCTCCA CGCACAGGTC GATTTCAGG TTGCTGACCG CCGAGCTGAC 1140
CGCGGTGTC GACTTGCACCA GGATCCGCGC AGCGGAGGAA ATCGAACCGG AGGCAGATGAC 1200
1210 1220 1230 1240 1250 1260
CTGGAGGAAC ATGTTCACGT GATTCAAGGTT ATGAATAGGC ATCCCTTATT CCTTTTATTG
GGTGGCGCGT GCCGCTTCCC TTGA 1284

Fig. 7F

92/133

Sequence: 34B12 ORF 1 (L-S) PROTEIN From: 1 To: 427

10 20 30 40 50
.....
MARARPCVSI SVTRCSTASL TCASRATTRW WSVACRKVST AWPMPMARSW
RWPIRAIDSACNSIPSRSFSPPTASVCWRTLYSGAARWRSRSAFGPERRC
AVSTEARLPGRRIVETLAAQFAQALAGAFEKATEAALGFQRGVVVAIHLG
VDAARFVQFAEDCQGTVAQAFLDEIMRRDAPSDAGFHQTQHVVEVFHEEY
LVADRPQQVRLMLPGAATEADLPVIGQARDAVQGGIAQRVLRMGDDERLGV
260 270 280 290 300
.....
AEHALVEAGDLQFLVDGDGDIDFRVVLDRRQAIGGRGAYQADHVEIVEQ
YAAHRIAERRRDGGVQQHPEIARTLVEIEGDVADQLLVQQAHHVRDQAK
RLLGGFDLVAVPTDQLHAQVDFQVADRRADRGVRLAQDPRSGGNRTGGDD
LEEHVHVIQVMNRHPLFLLGGACRFP 427

Fig. 7G

0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100

93/133

Sequence: 34B12 ORF 2 From: 1 To: 1035

10 20 30 40 50 60
ATGCCTATTC ATAACCTGAA TCACGTGAAC ATGTTCTCC AGGTCACTGC CTCCGGTTG 60
ATTTCTCCG CTGCGCGGAT CCTGCGCAAG TCGCACACCG CGGTCAGCTC GGCGGTCAAG 120
AACCTGGAAA TCGACCTGTG CGTGGAGCTG GTCCGTCGGG ACGGCTACAA GGTCGAACCC 180
ACCGAGCAGG CGCTTCGCCT GATCCCTTAC ATGCGCAGCC TGCTGAACTA CCAGCAGCTG 240
ATCGGCGACA TCGCCTTCAA TCTCAACAAG GGTCCGCGCA ATCTCCGGGT GCTGCTGGAC 300
310 320 330 340 350 360
ACCGCCATCC CGCCGTCGTT CTGCGATAACG GTGAGCAGCG TACTGCTCGA CGATTCAAC 360
ATGGTCAGCC TGATACGCAC CTCGCCCCGC GATAGCCTGG CGACGATCAA GCAGGACAAC 420
GCGGAAATCG ATATGCCAT CACCATCGAC GAGGAACCTGA AGATCTCCCG CTTCAACCAG 480
TGCCTGCTCG GCTACACCAA GGCCTTCGTC GTCGCCCCATC CGCAGCACCC GTTGTGCAAT 540
GCCTCCCTGC ACAGCATCGC GAGCCTGGCC AATTACCGGC AGATCAGCCT CGGCAGCCGC 600
610 620 630 640 650 660
TCCGGGCAGC ATTGAAACCT GCTGGGCCG GTCAGCGACA AGGTGCTCTT CGTGGAAAAC 660
TTCGACGACA TGCTGCGTCT GGTGAAAGCC GGCCTCGGAT GGGGCATCTC GCCGCATTAT 720
TTCGTCGAGG AACGCCCTGCG CAACGGTACC CTGGCAGTCC TCAGCGAACT GTACGAACCG 780
GGCAGGATCG ACACCAAGGT GTATTGCTAC TACAACACCG CGCTGGAATC CGAGCGCAGC 840
TTCCGTGCGT TTCTCGAAAG CGCCCGCCAG CGCCTGCGCG AACCTGGGCCG CCAGCGTTTC 900
910 920 930 940 950 960
GACGATGCGC CGGCCTGGCA ACCGAGCCTC GGTCGAAACT GCGCAGCGCC GCTCAGGCC 960
GAAGGGCGTC CGCGACCGCC AACCGGCCGC ACCAGAGTAG AGCGTTCTCC AGCAGACGCT 1020
GGCCGTGGGT GGTGA 1035

Fig. 7H

94/133

Sequence: 34B12 ORF 2 PROTEIN From:: 1 To: 344

10 20 30 40 50 60
MPIHNLNVN MFLQVIASGS ISSAARILRK SHTAVSSAVS NLEIDLCVEL VRRDGYKVEP 60
TEQALRLIPY MRSLLNYQQL IGDIAFNLNK GPRNLRVILD TAIPPSFCDT VSSVLLDDFN 120
MVSLIRTSPA DSLATIKQDN AEIDIAITID EELKISRPNQ CVLGYTKAFV VAHPQHPLCN 180
ASLHSIASLA NYRQISLGSR SGQHSNLLRP VSDKVLFVEN FDDMLRLVEA GVGWGIAPHY 240
FVEERLRNGT LAVLSELYEP GgidTKVYCY YNTALESERS FRRFLESARQ RLRELGRQRF 300
310 320 330 340 350 360
DDAPAWQPSL GRNCAAPLRP EGAPRPPTRR TRVERSPADA GRGW 344

Fig. 71

95/133

Sequence: 34B12 ORF 1 From:: 1 To: 759

10 20 30 40
ATGCGGCGAG ATGCCCATC CGACGCCGGC TTCCACCAGA 40
CGCAGCATGT CGTCGAAGTT TTCCACGAAG AGCACCTTGT 80
CGCTGACCGG CGCGAGCAGG TTCGAATGCT GCCCGGAGCG 120
GCTGCCGAGG CTGATCTGCC GGTAAATTGGC CAGGCTCGCG 160
ATGCTGTGCA GGGAGGCATT GCACAAACGGG TGCTGCGGAT 200
210 220 230 240
GGGCGACGAC GAACGCCTTG GTGTAGCCGA GCACGCAC TG 240
GTTGAAGCGG GAGATCTTCA GTTCCCTCGTC GATGGGTGATG 280
GCGATATCGA TTTCGCGTT GTCCTGCTTG ATCGTCGCCA 320
GGCTATCGGC GGGCGAGGTG CGTATCAGGC TGACCATGTT 360
GAAATCGTCG AGCAGTACGC TGCTCACCGT ATCGCAGAAC 400
410 420 430 440
GACGGCGGGA TGGCGGTGTC CAGCAGCACC CGGAGATTGC 440
GCGGACCCCTT GTTGAGATTG AAGGCGATGT CGCCGATCAG 480
CTGCTGGTAG TTCAAGCAGGC TGCGCATGTA AGGGGATCAGG 520
CGAAGCGCCT GCTCGGTGGG TTCGACCTTG TAGCCGTCCC 560
GACGGACCAAG CTCCACGCAC AGGTGATTT CCAGGTTGCT 600
610 620 630 640
GACCGCCGAG CTGACCGCGG TGTGCGACTT GCGCAGGATC 640
CGCGCAGCGG AGGAAATCGA ACCGGAGGCG ATGACCTGGA 680
GGAACATGTT CACGTGATTG AGGTTATGAA TAGGCATCCC 720
TTATTCCCTT TATTGGGTGG CGCGTGCCGC TTCCCTTGA 759

Fig. 7J

96/133

Sequence: 34B12 ORF 1 S PROTEIN From:: 1 To: 253

10 20 30 40
MRRDAPS DAG FHQTQHVVEV FHEEHLVADR PQQVRMLPGA 40
AAEADLPVIG QARDAVQGGI AQRVLRMGDD ERLGVAEHAL 80
VEAGDLQFLV DGDGDIDFRV VLLDRRQAIG GRGAYQADHV 120
EIVEQYAAHR IAERRRDGGV QQHPEIARTL VEIEGDVADQ 160
LLVVQQAAHV RDQAKRLLGG FDLVAVPTDQ LHAQVDFQVA 200
210 220 230 240
DRRADRGVRL AQDPRSGGNR TGGDDLEEHV HVIQVMNRHP 240
LFLLLGGACR FP. 253

Fig. 7K

REPRODUCED BY HIGH SPEED FAX

pho34B12 ORF1 (L-S) SEQ ID NO:107

1 MARARPCVSI SVTRCSTASL TCASRATTRW WSVACRKVST AWPMPMARSW
51 RWPIRAIDSW ACNSIPSRSF PPTASVCWRT LYSGAARWRS RSAFGPERRC
101 AVSTEARLPG RRIVETLAAQ FAQALAGAFE KATEAALGFQ RGVVVAIHLG
151 VDAARFVQFA EDCQGTVQAQ FLDEIMRRDA PSDAGFHQTQ HVVEVFHEEY
201 LVADRPQQVR MLPGAATEAD LPVIGQARD A VQGGIAQRVL RMGDDERLGV
251 AEHALVEAGD LQFLVDGDGD IDFRVVLLDR RQAIGGRGAY QADHVEIVEQ
301 YAAHRIAERR RDGGVQQHPE IARTLVEIEG DVADQLLVQ QAAHVRDQAK
351 RLLGGFDLVA VPTDQLHAQV DFQVADRRAD RGVRLAQDPR SGGNRTGGDD
401 LEEHVHVIQV MNRHPLFLLL GGACRFP*

Fig. 8

phoB12 ORF2 SEQ ID NO: 108

1 MPIHNLNHVN MFLQVIASGS ISSAARILRK SHTAVSSAVS NLEIDLVEL
51 VRRDGYKVEP TEQALRLIPY MRSLLNYQQL IGDIAFNLNK GPRNLRVLLD
101 TAIPPSFCDT VSSVLLDDFN MVSLLRTSPA DSLATIKQDN AEIDIAITID
151 EELKISRFNQ CVLGYTKAFV VAHPQHPLCN ASLHSIASLA NYRQISLGSR
201 SGQHSNLLRP VSDKVLFVEN FDDMLRLVEA GVGWGIAPHY FVEERLRNGT
251 LAVLSELYEP GGIIDTKVYCY YNTALESERS FRRFLESARQ RLRELGRQRF
301 DDAPAWQPSL GRNCAAPLRP EGAPRPPTTR TRVERSPADA GRGW*

Fig. 9

36A4 SEQ ID NO: 109

1 AAGGGTTTG GCGGGGTCA T CCGAGTGACC CTGAGCATGC TCCTGGCGAT
51 CTTCTTGTG C GTGCTGCTGG CGCCGGTGC C CATGCTGTT C CACACCCGCT
101 TCGTGCTGGC CGCCTTCCTC GGCTGGTC

Fig. 10

36A4 SEQ ID NO:110

1 KGFGGVIRVT LSMLLAIFLS VLLAPVRMLF HTRFVLAALF GW

Fig. 11

contig 2507 SEQ ID NO: 111

1 CTAATGGGGC AAGCTGAAGA CGCCGTTCAA GCTGAGCTTC TATCACCAGG
 51 GCATGCACTT CGACACGCCG GTGAAGATCA ACGAGGTGAC CGCTACCACG
 101 GTCAAGCCGA TCAAGTACGA TCGCACCAAG TTCGATTCG GATCCCTGAA
 151 GTTCGACGAG AATGCCACCA AGGATCTCGG CTATGCCGGT TTCCCGTGC
 201 TCTATCCGAT CAACAAGGCC GACAAGCAGG ACGAGATCGC CACCTTCCTT
 251 GGCGCAGACT ACTTCCGCGT GGTCGCAAG GGCCAGGTCT ACGGTCTGTC
 301 GGCGCGCGC CTGGCGATCG ATACCGCGCT GCCTTCGGGC GAAGAGTTCC
 351 CGCGCTTCCG CGAATTCTGG ATCGAGCGGC CGAAGCGCAG GACAAGCAAC
 401 TGGTGATCTA CGCCCTGCTC GACTCGCCGC GGGCCACCGG CGCCTACCGC
 451 TTCGTGCTGC GTCCGGCAA GGATGCGGTG ATGGATGTCC AGGCCCGGT
 501 GTTCCTCCGC GACAAGGTCA GCAAGCTGGG CCTGGCGCCG CTGACCAAGCA
 551 TGTACCTGTT CGGCTCCAAC CAGCCGTCCG AGCAGCACAA CTTCCGGCCC
 601 GAGCTGCATG ACTCCAGCGG CCTGCAGATC CATGCCGGCA ACGGCGAGTG
 651 GCTGTGGCGT CCGCTGAACA ATCCGAAGCA CCTGTCGGTG AGCACCTTC
 701 GCGTGGAGAA CCCGAAAGGC TTCGGGCTGC TCCAGCGCGG CCGCGAGTTC
 751 TCCCCTACG AAGACCTGGA TGACCGCTAC GACCTGCGTC CGAGTGCCTG
 801 GATCGAGCCG AAGGGCGACT GGGGCAAGGG CACCGTGGAA CTGGTGGAAA
 851 TCCCAGCCCC GGACGAAACC AACGACAATA TCGTCGCGTT CTGGAACCCCC
 901 GAGACCCAGC CTGAGGTCTGG AAAGCCGCTG GACTTCGCCT ACCGCCTGCA
 951 CTGGACCATG GATGAAGACG AGCTGCACGA CCCGAAATCC TCCTGGGTCA
 1001 AGCAGACCAT GCGCTCGGTG GCGACGTGA AGCAGAAGAA CCTGATCCGC
 1051 CAGCAGGACG GCAGCACCGC CCTGGTCGTC GACTTCGAAG GGCCGGCCCT
 1101 GAAGGACCTG GCGCCGGACG CGCCGGTGAC CACCCAGGTC AGCACCGACA
 1151 GCAACGCCGA GGTGGTGGAG AACAGCCTGC GTTACAACCC GGTCTGAAA
 1201 GGCTGGGCC TGACGCTGCG GATCAAGGTC AAGGATCCGA AGAAGCCGGT
 1251 GGAAATGCGC GCGGCGCTGG TCGACGAGGC GCAGAAGCCA CTGAGCGAAA
 1301 CCTGGAGCTA TCAGCTGCCT GCCGATGAAT AACCCATCCA CTACGAAAGC
 1351 ACCGCTGGCC GACTACCTCG CTCATCTTCC CCTGGCGGAA GAGGAGCGGG
 1401 AGCGCTTGG CGAGTCCGCT TCCTTCTCCG AGCTGCACGC TCGCCTGGCG
 1451 GGAGCGGAAG GCGCCGCTGC CGATGCCGGG GGCATCCCG CCCTGGCCTC
 1501 GGTACGCGCC CGCCTGCAGC TGGGCACCCC TGAGCTGGAC GACGCCGAGA
 1551 TGTCGGCGT CGACGCCAG GGTGCGACCT TCCTCAAGAT TTCCCCGCGC
 1601 ATCCGCCGTA CCAAGGTGAT TCCCAGGCC TGGCGCACCA ACATCCTGGT
 1651 GCGCGGCTGG CGTCGGCTGA CGGACGCGAG CAACCCGCC AAGCCCAAGC
 1701 GTGCCCTGCC GCGGGCCCGC TGGCAGCGGG TCGGCTCGCT GCGCCGGTTC
 1751 ATCCCTGCTGT TGTTGATGCT GGCACGACCC TCGGTCGCCA CCTACTACAT
 1801 GAAAGGCATC CTGCCCTACC AGGGCTGGGC CTTCGTCGAC CTGGAGGAGC
 1851 TGGCCCAGCA GAGCCTGCTG GATACCGTCC AGCAGGTGCT GCCCTATGTC
 1901 ATCCAGTTCG GCATCCTGGC GCTCTCGCG ATCCCTCTCT GCTGGGTCTC
 1951 GGCCGGCTTC TGGACCGCGC TGATGGCTT CTGGGAGCTG CTCACCGGGC
 2001 GTGACCGCTA CGGGATCTCC GGCAGCAGCG CGGGCAGCGA GCCGATCGCC
 2051 GCGGACGCCG GCAACGGCGAT CGTCATGCCG ATCTGCAACG AAGACGTGCC
 2101 GCGGGTATTC GCCGGCCTGC GGGCGACCGT CGAGTCGATG GCCGCCACCG
 2151 GCGAGATGGA GCGCTTCGAC TTCTTCGTC TCAGCGACAC CAACGACCCG
 2201 GATATCGCCG TCGCCGAGCA GCAGGCCTGG CTCGAGCTGT GCCGCGAGAC
 2251 CAAGGGCTTC GGCAAGATCT TCTACCGTCG CGGCCGGCGC CGGGTGAAGC
 2301 GCAAGAGCGG CAACATCGAC GACTTCGTC GGCGCTGGGG CGGCAGACTAC
 2351 CGCTACATGG TGGTGTGGA CGCCGACAGC GTGATGAGCG GCGACTGCCT

Fig. 12A

2401 GGCCAAGCTG GTACGCCTGA TGGAGGCCAA TCCTGAGGCG GGGATCATCC
 2451 AGACCGCGCC GAAGGCTCCG GCATGGACAC CCTGTATGCG CGCATGCAGC
 2501 AGTTCGCCAC CCGCGTCTAC GGCCCCTGTG TCACCGCCGG CCTGCACCTTC
 2551 TGGCAACTCG GCGAGTCGCA CTACTGGGC CACAACGCGA TCATCCGCAT
 2601 GCAGCCCTTC ATCGACCACT GCGCCCTGGC GCCGTTGCCG GGCAAGGGCT
 2651 CGTTCGCCGG CGCGATCCGT TCCCACGACT TCGTCGAGGC TGCGTTGATG
 2701 CGCCTTGCCG GCTGGGGCGT GTGGATCGCC TACGACTTCG ACGGCAGCTA
 2751 CGAAGAACTG CGGCCGAACC TGCTCGACGA ACTCAAGCGC GACCGCCGCT
 2801 GGTGCCACGG CAACCTGATG AACTCCGCC TGTTCCCTGGT CAAGGGCATG
 2851 CACCCGGTGC ACCCGCGGGT GTTCCCTCAC GGGGTATGT CCTACCTGTC
 2901 GGCGCCGTTG TGGTTCTTCT TCCTGGTGT TTCCACCGCG CTGCTGGCGG
 2951 TGCACCAACT GATGGAGCCG CAGTACTTCC TGGAAACCGCG GCAGCTGTC
 3001 CCGATCTGGC CGCAGTGGCA TCCGGAGAAG CCCATCGCGT TGTTCTCCAC
 3051 CACCCGTGACC CTGTTGTTCC TGCCCAAGCT GCTCAGCGTA ATGCTGATCT
 3101 GGGCCAAGGG CGCCAAGGGT TTCGGCGGGG TGATCCGGT GACCCCTGAGC
 3151 ATGCTCCTGG AGATGTTCTT CTCGGTGTG CTGGCGCCGG TGCGCATGCT
 3201 CTTCCACACC CGCTTCGTGC TGGCCGCCCT CCTCGGCTGG TCGGTGCAGT
 3251 GGAACTCGCC GCAGCGCGAC GACGACGCCA CGCCCTGGAG CGAGGCGATC
 3301 CGCCGGCACG CAATGCAGAC CCTGCTGGGT ATCGCCTGGA CCCTGCTGGT
 3351 GGCCCTGGTC AACCCCGCGT TCCTGTGGTG CCTGTCGCCG ATCGTCGGTT
 3401 CGCTGATCCT GTCGATCCCG GTATCGGTGA TCTCCAGCCG GGTGAAGCTG
 3451 GGCCCTGGGG CCCGCTACGA AAAGCTGGTC CTGATCCCAG AGAGTACGAC
 3501 ACGCCGCGCG ACTGCGCGCC ACCGACGAGT ACACCTACGA GAACCGCTGG
 3551 CATGCGCTCA AGGATGGCTT CCTCAAGGCC GCCGTCGATC CGTTGCTCAA
 3601 CGCCCTGGCC TGGCCATGG GCACGGCTCG CCACAACCGT GCGCAGGCCA
 3651 TCGAGACGGT GCGTGGCGAG CGTATCGGCA AGGCCATCGA TAAGGGCCCG
 3701 GAACAGCTG ACGGCGCCAC GCGCCCTGGCT CTGTTGAGTG ACCCGGTAGC
 3751 ACTTTCGCGC CTGCATACGC GGGTCTGGGA AGAGGACCGC GACGACTGGC
 3801 TCGGCCGCTG GCGCAAGGCC GAGGCGGACG ACCCCCCACGC CGCCAGCGTA
 3851 CCGCTGGCCC AGGTAGTGCC CGGCGACGCC GGCCTGCTGC CGGCCGCCCA
 3901 GTCCTGATCC CATGCCCGC GCGGAACGCC GCCGGGGGCA TGGGTCTGTT
 4001 TCTTGCTGT TTTCCCCGTG CGGCGCTGCT GTTACCCCTGC GCCGGCAATC
 4051 CAGAAAGTCT CGTATCGTTC GCCAGCTGAG GTACTATCGG CCGCCTTTG
 4101 CGCAGCCGGT CATGGCCTGC TGCCCGCCCG GGACGGCGAC ACGACGAGAG
 4151 CATCCGTTG ACAGACTGTGT TTCTAAGACT GCTGGGGATT GGGGAATGAA
 4201 AAAGTATCTT GCTTCATTGG TTCTGGCGT CTGCGCCCTG GTGGCGTGG
 4251 CTTCGGTCCA GGCAGGCCGGC GCGGTGGAGG ACGCGGTCAA GCGCGGCACC
 4301 CTGCGGGTCG GCATGGACCC GACCTACATG CCGTTCGAGA TGACCAACAA
 4351 GCGTGGCCAG ATCATCGGCT TCGAAGTCGA CCTGCTCAAG GCCATGGCCA
 4401 AGTCCATGGG CGTCAAGCTG GAGCTGGTCT CCACCAGCTA CGACGGCATC
 4451 ATCCCGGCCG TGCTGACCGA CAAGTCGAC ATGATCGGCT CGGGCATGAC
 4501 CCTGACCCAG GAGCGCAACC TGCGCCTGAA CTTCTCCGAG CCCTTCATCG
 4551 TGGTCGGCCA GACCCCTGCTG GTGCGCAAGG AACTGGAAGG CAAGATCAAG
 4601 TCCTACAAGG ACCTGAACGA TCCGCAAGTAC AGCATCACCT CGAAGATCGG
 4651 CACCAACGGT GAGATCGTT CCCGCAAGCT GATCAGCAAG GCCAAGTACC
 4701 ACGGCTTCGA CAAAGAGCCG GAAGCGGTGA TGGACGTTGGT CAACGGCAAG
 4751 GCCGACGCCCT TCATCTACGA CTCGCCCTAC AACGTGGTGG CGGTGAGCAA
 4801 GTTCGGCGCC GGCAAGCTGG TCTACCTCGA CCAGCCGTTT ACCTACGAGC
 4851 CGCTGGCGTT CGGCCTGAAG AAAGGCGACT ACGACAGCAT CAATTTCATC
 4901 AACAACTTCC TCCATCAGAT CGCGAAGAC GGCACCTATC AGCGCATCCA

Fig. 12B

4951 CGACAAGTGG TTCAAGAACCA CCGAGTGGCT GAAGGAAATG GAATGAACCG
 5001 CTGACGGCCC CCGCGAAGGG GGCGTCGTA CCTGCGCATT CCATCGTCG
 5051 AGAGAGTTTC CGTGACCAAG AAGAAACGTT CCGTCTGGCC CTGGCACCTG
 5101 CTGACCGGGC TGATCCTGCT GGTATGGCC TGGGCGCTGT GGTTCTCCAC
 5151 CTCGCTGATT TCCTATGAAA TGGCGTGGGA CCGCGTTTCC GAGTACTTCG
 5201 CTACCAAGGCC GAGGAGCCGT TACGGGCCA CGAGATCGGC CGGGTCGAGG
 5251 CTATCGAGGA ACAGGGCAGG GACGCCGCG TCACGCTGCT TGGCGAGACG
 5301 GCGAGAACCA GGTGCGTGCAC GTTGCCCAGG ACAGCCTGCA ATTCTCCGAA
 5351 GCGACGACGT GGGCGAGGGC GACGCCGTCG GGGTGACCCG CCACCTGGGCC
 5401 GCCGGCACTG CTCTGGGGCC TGTGGACAC CCTCTGGCTA TCGCTGGTGT
 5451 CCGGTGCCAT CGGTCTGGCT ATCGGCGTGG TCGCCGGCCT CTGCCGGCTG
 5501 TCGAAGAACCA CGACCCCTGCA CGACCTGTCG ACGATCTACG TCGAGCTGGT
 5551 GCGCGGCACG CCGTTGCTGG TGCAAGATCTT CATCTTCTAC TTCTTCATCG
 5601 GCACCGTGCT CAACCTGTCC CGCGAGTTCG CCGGGGTTGC GGCGCTGGCG
 5651 CTGTTCACCG GCGCCTACGT GGCGAGATC ATCCGGGCG GCGTGCAGTC
 5701 CATCGCCCGC GGACAGAACCG AGGCCGCCCG CTCCCTGGGC CTGAACGCCG
 5751 GCCAGTCGAT GCGCTACGTG ATCCTGCGC AGGCTTCAAG CGCGTGCCTGC
 5801 CGCCGCTGGC CGGGCAGTTC ATCAGCGTGG TCAAGGACAC CTCGCTGGTC
 5851 TCGGTGATCG CCATCACCGA ACTGACCAAG AGCGGCCCG AGGCAGATCAC
 5901 CCACTTCGTT CTCCAACCTTC GAGATCTGGT TTCTGCGTCG CCGCGTTGTA
 5951 CCTGCTGTT AACCTGCCCTTTCGACAT GGCATCCCGA CTGGAGCGGA
 6001 GGCTCGGACA AAGTGATTGA AGTACCGAAC CTGCTGAAGG TCTTCGATAC
 6051 CCGCGGCCAG GTAGTGCAGCG CGGTGGACGA CGTGAGTACC CGCGTGGCCA
 6101 GGGGCGAGGT ACTGGTGGTG ATCGGTCCGT CCGGTTCCGG CAAGTCGACC
 6151 TTCCCTGCGCT GCCTGAACGG CCTGGAGGAG TTGACGAAG GCTCGGTGAG
 6201 CATCGACGGC GTGACCTGG CCGACCCGAG GACCGACATC AATGCCCTACC
 6251 GCGCGAAGT CGGCATGGTG TTCCAGCATT TCAACCTGTT CCCGCACATG
 6301 ACCGTGCTCG AGAACCTCTG CCTGGCCCAA CGCGTGGTGC GCAAGCGCGG
 6351 CAAGGCCGAG CGCGAGGCCA AGGCGCGGGC GCTGCTGGCC AAGGTGGCA
 6401 TCGGGCAGAA GGGCGACGAA TATCCCTCGC GCCTGTCGG CGGCCAGCAG
 6451 CAGCGCGTGG CGATCGCTCG CGCGTGTGTC ATGGACCCCA AGGTGATGCT
 6501 GTTCGACGAA CCGACCTCGG CGCTCGATCC GGAGATGGTC GGCGAAGTCC
 6551 TCGACGTCA TGAAGACCTG GCCGTGGAAG GCATGACCAT GGTCTGCGTG
 6601 ACCCACGAGA TGGGCTTGC CGCGAAGTG GCGACCGCG TGCTGTTCTT
 6651 CGACCAACGGC AAGCTGCTGG AGGACCGGCC GCGGGCGCAG TTCTCGACA
 6701 ATCCGCAGGA CCCGCAGGCC CAGGCCTTCC TCCGCCAGGT CCTCTAGTAC
 6751 CGCGCTAGGC GAACGGCTTG CCCGGCGGGC GCAAGGAGCGA CGTGGACTC
 6801 TGCCGCGCGG CCGGCTGGAT ATCGTTGTCC TCCAGCCAGT CCAGCGCCCA
 6851 TTGCGCGCAGG CGCTCGTTCT GGTAGCGGTA CCAGTCCCTGC AACAGTTCCG
 6901 GGTACTCCAT CAGAGAGTGC TTGAAGGCCT TGAACGGCTT GCGGCTCTGC
 6951 AGCGCGTTG

Fig. 12C

101/133

23A2 DNA SEQ ID NO:112

1 CGAGGGTTCC GTCTACGAAG GCACCGGCTC GGTCAACCATC CGCGCCGTGT
51 TCCCCAACCC GAACAACGAG CTGCTCCCCG GCATGTTCGT TCACGCGCAG
101 TTGCAGG

Fig. 13

23A2 peptide SEQ ID NO:113

1 EVSVYEGTGS VTIRAVFPNP NNELLPGMFV HAQLQ

Fig. 14A

SEQ ID NO:148

DNA flanking the 23A2 locus.

mexA partial sequence, mexB partial sequence

1 ggccaggcaa acgcgatggc caccgtgcaa cagctcgacc cgatctacgt cgacgtcacc
61 cagccgtcca ccgcctgtt gcgcatgcgc cgcgaaactgg ccagcggcca gttggagcgc
121 gccggcgaca acgctgcgaa ggtctccctg aagctggagg acggtagcca ataccgctg
181 gaaggccgccc tcgaattctc cgaggtttcc gtcgacgaag gcaccggctc ggtcaccatc
241 cgcgcgtgt tccccaaccc gaacaacgag ctgctcccg gcatgttcgt tcacgcgcag
301 ttgcaggaag gcgtcaagca gaaggccatc ctgcgtccgc agcaaggcgt gacccgcgac
361 ctcaaggggcc aggctaccgc gctgggtgtt aacgcgcaga acaaggtcga gctgcgggtg
421 atcaaggccg accgggtat cggcgacaag tggctggtca ccgaaggcct gaacgcggc
481 gacaagatca ttaccgaagg cctgcagttc gtgcagccgg gtgtcgaggt gaagaccgtg
541 cggcgaaga atgtcgctc cgccgacaag gccgcgcgcg ctccggcgaa aaccgcacgc
601 aagggtgtat caaggggatt cgtaatgtcg aagttttca ttgataggcc catttcgcg
661 tgggtgtatcg ccttgggtat catgctcgcg ggcggcctgt cgatcctcaa tctgcggc
721 aaccagtacc cggccatcgcc cccgcggcc atgcgcgtgc aggtgagcta cccggcgcc
781 tcggccgaga cggcgcagga caccgtggc caggtgatcg agcagcagat gaacgggatc
841 gacaatctgc gctacatctc ctgcggagagt aactccgacg gcagcatgac catcaccgtg
901 accttcgaac agggcaccga cccgcacatc gcccagggtcc aggtgcagaa caagctcaa
961 ctggccaccc cgctgctgcc gcaggaagtg cagcgcagg ggatccgg

Fig. 14B

SEQ ID NO:149

PA14 mexA

G QANAMATVQ QLDPIYVDVT QPSTALLRMR RELASGQLER AGDNAAKVSL KLEDGSQYP LEGRLEFSE
VSVDEGTGS VTIRAVFPN PNNELLPGM FVHAQLQEG VKQKAILAP QQGVTRDLK GQATALVVN
AQNKVELRV IKADRVIGD KWLVTTEGLN AGDKIITEG LQFVQPGVE VKTVPAKNV ASAQKADAA PAKTDSKG

Fig. 14C

SEQ ID NO:150

PA14 mexB

MSKFFIDRPIFAWVIALVIMLAGGLSILNLPVNQYPAIAPPAIA
VQVSYPGASAETVQDTVVQVIEQQMNGIDNLRYISSESNSDGSMTITVTFEQGTD PDI
AQVQVQNLQLATPLLPQEVRQGIR

Fig. 14D

PAO1 Phenazine operon SEQ ID NO:114

1 GCAAGCTCAA CTCCAGCAAC AAGGCGGAGG CCACCATGAA GGCTTACGCC
 51 ATCGGCCTGC TCAACTGAAT CGACGCCTCG TCGCCTAGCG AGGCCGCCGC
 101 GCAAGCGTCC GGCCATTACAC CGAATGGCCG GATAGCGTTT GCGCCGGTCG
 151 CCTGAGCGCA CGCTTCCCAC CGGCAGCGTT TCCCCGCTGC CCCCTTCGCC
 201 ATTGCGCCCG TCCTCATGTT GTCCGGACGC TAGTCGAACT TTCCGGCGC
 251 CTGGCAAACC GGCCAAAGAA TAGAACGAA TCGATGCCA CACCTTAAT
 301 TTTTAAGGGT TTTTCTTTT CAAAAACCGT TATTAAGTTT TCCCCTTAA
 351 ATCTTGGTAC AACTGGGTC AGGCGAAACT TCGGTATGC CATTGGCAT
 401 TAGTTAAACT TTGAGACTCT CCAAGCGGG A TTTTGCCG GAACAGCTTC
 451 ACGGCATTC TCCGCTTCA TCCCAGATTT TCTTCCGTT ATGATTCCAG
 501 TCGATTGAA CTGCCGGAGT TCCCACCATT CGAGATTACC AACGTTGAA
 551 AGGGTTAAC GACAACCTGG AATTGCGTCG GCGCAACCGT GCCACGGTCG
 601 AGCACTACAT GCGCATGAAG GGGGCCGAAC GGTACAGCG GCACAGCTG
 651 TTCGTCGAGG AGGCTGCGCC GGCAACTGGA CCACGGAAAG CGGCGAACCC
 701 CTGGTTTCC GGGGCCATGA GAGCCTCAGG CGGCTCGCCG AGTGGCTCGA
 751 GCGCTGCTC CCCGACTGGG AGTGGCACAA CGTGCAGGATC TTCGAGACCG
 801 AGGATCCGAA CCACTTCTGG GTGAGTGC ACGGGCGCGG CAAGGCGCTG
 851 GTCCCAGGGT ATCCGCAGGG CTATTGCGAG AACCACTACA TCCATTCTT
 901 CGAACTCGAG AACGCCGGA TAAAACGCAA TCGCGAGTTC ATGAACCGA
 1001 TGCAGAAATT GCGTGCATTG GGAATAGCCG TTCCACAAAT AAAACGTGAC
 1051 GGTATTCCA CCTGATTAAT GTCTATTCCA ATTCAAGAGG AGATATGACG
 1101 ATGCTCGATA ATGCCATTCC TCAAGGTTTC GAAGACGCCG TGGAGTTGCG
 1151 CAGGAAGAAT CGCGAGACGG TGGTCAAGTA TATGAACACC AAAGGCCAGG
 1201 ATCGCCTGCG CCGCCATGAA CTTTCTGCG AGGACGGCTG TGGCGGTTA
 1251 TGGACCACCG ATACCGGCTC GCCCCATCGTC ATTCTGGCA AGGACAAGCT
 1301 GGCCGAGCAC CGGGTGTGGT CGCTGAAATG CTTCCCGGAT TGGGAGTGGT
 1351 ACAACATCAA GGTCTCGAG ACCGACGATC CCAACCACTT CTGGGTCGAG
 1401 TGCGACGGCC ACGGCAAGAT CCTCTTCCCC GGCTATCCCG AGGGCTACTA
 1451 CGAGAACAC TTCTGCATT CCTTCGAGCT GGACGACGGC AAGATCAAGC
 1501 GCAACCGCGA ATTCAATGAA GTCTTCCAGC AATTGCGCGC CCTGAGCATT
 1551 CCGGTCCCCG AGATCAAACG CGAAGGCATT CCCACCTGAG GCCATCTGG
 1601 AAGGGGTGAA CTATGGACGA TCTATTGCAA CGCGTACGGC GCTGCGAACG
 1651 GCTGCAGCAA CCCGAATGGG GCGATCCGTC GCGCCTGCGC GACGTGCAGG
 1701 CGTACCTGCG CGGCAGTCCG GCGCTGATCC GCGCCGGCGA CATCCTGGCC
 1751 CTGCGCGCGA CCCTGGCGCG GGTGCCCCGC GGCGAGGCAGC TGGTGGTGCA
 1801 GTGCGGCAGAC TGCGCCGAGG ACATGGACGA CCACCATGCC GAGAACGTGG
 1851 CGCGCAAGGC CGCCGTGCTG GAACTGCTGG CGCGCGCCCT GCGCCTGGCC
 1901 GGCCGGCGGC CGATAGATCC GCGTCGGCG CATCGCCGGG CAGTACGCCA
 1951 AGCCGCGTTC CAAGCCGCAC GAGCAGGTGC GCGAGCAGAC CCTGCCGGTC
 2001 TATGCGGGCG ACATGGTCAA CGGCCGCGAG GCCCATGCCG AACAGGCCG
 2051 GGCGATCCG CAGCGGATCC TCAAGGGCTA TGCAGGGCG CGCAACATCA
 2101 T

3E8 sequence SEQ ID NO:115

1 CGGCGCCGAG GATCCGCTGT TCGAGTTAGG CGCAAGCGTC CGGCCATTCA
 51 CGGAATGGCC GGATAGCGTT TGCGCCGGTT GCTTGAGCGC AGCTTCCCAC
 101 CGGCAGGGTT TCCCCGCTGC CCCTTTCGCC ATTGCGCCGT CCTCTTGTG
 151 TCCGGCACGC TAGTGCAACT TTCCGGACGC TTGGCAAACC GGCCAAAGAA
 201 TAGAACGGAA TCGATGCCCC ACACCTGTAA TTTTTAAGGG GTTATGGCTA
 251 TTGCAAAAAA GCGTTTATAA GTTTGCCCCC TGTCAAATCT GGTTACAACT
 301 GGGTTTCAGG CGAAACATTC GGTATGGCA ATTGGCATT AGTTGAAACT
 351 TTGGAGACGC TCCGAAGCGG GCAACTTTG CCCGGAAAAA GTTTCACGGC
 401 AATTTTCCG GCCGTGTCATC CCGATGTCTT CTTTCCAGTA TGGATGCCAG
 451 TCGATTGAA CTGGCGGAGA TTTCGACCAT GCGAGAGTAC CAACGGTTGA
 501 AAGGGTTTAC CGACAACCTG GAATTGCGGC GGCGCAACCG TGCCACGGTC
 551 GAGCACTACA TGCGCATGAA GGGGGCCGAA CGGTTGCAGC GGCACAGCCT
 601 GTTCGTGAG GACGGCTGCG CCGGCAACTG GACCACGGAA AGCGGCGAAC
 651 CCCTGGTTT CCGGGGCCAT GAGAGCCTCA GGCGGCTCGC CGAGTGGCTC
 701 GAGCCTGCT TCCCCGACTG GGAGTGGCAC AACGTGCGGA TCTTCGAGAC
 751 CGAGGATCCG AACCAACCTCT GGGTCGAGTG CGACGGCGC GGCAAGGC
 801 TGGTCCCCGG GTATCCGCAG GGCTATTGCG AGAACCACTA CATCCATTCC
 851 TTCGAACCTCG AGAACGGCCG GATAAAACGC AATCGCGAGT TCACGAACCC
 901 GATGCAGAAA TTGCGTGCAT TGGGAATAGC CGTTCCGCAA ATAAaACGTG
 951 ACGGCATTCC CACCTGATTA ATGATTATTCA ATTCAAGA GGAGATATGA
 1001 CGATGCTCGA TAATGCTATT CCCCAGGTT TCGAAGACGC CGTGGAGTTG
 1051 CGCAGGAAGA ATCGCGAGAC GGTGGTCAAG TATATGAACA CCAAAGGCCA
 1101 GGATCGCTG CGCCGCCATG AACTTTCGT CGAGGACGGC TGTGGCGTT
 1151 TATGGACCAC CGATACCGGC TCGCCCATCG TCATTCTGG CAAGGACAAG
 1201 CTGGCCGAGC ACGGGGTGTG GTCGCTGAAA TGCCTTCCCG GATTGGGAGT
 1251 GGTACAACAT CAAGGT

Fig. 16A

3E8 SEQUENCE TAG SEQ ID NO:160

1 tatggatgcc agtcgattcg aactggcgga gattgcacc atgcgagagt accaacgggt
 61 gaaagggttt accgacaacc tggaaattcg cgccgcacac cgtgccacgg tcgagcacta
 121 catgcgcatg aaggggcccg aacggttgca gcggcacagc ctgttcgtcg aggacggctg
 181 cgccggcaac tggaccacgg aaagcggcga acccctgggtt ttccggggcc atgagagcct
 241 caggcggctc gccgagtggc tggagcgtcg ctccccgac tggagtgcc acaacgtgcg
 301 gatcttcgag accgaggatc cgaaccacct ctgggtcgag tgcgacgggc gcccgaaggc
 361 gctggtcccg ggttatccgc agggctattg cgagaaccac tacatccatt cttcgaact
 421 cgagaacggc cggataaaac gcaatcgca gttcacgaac ccgatgcaga aattgcgtgc
 481 attggaaata gccgttccgc aaataaaacg tgacggcatt cccacctgat taatgattat
 541 tccaattcaa gaggagatat gacgatgctc gataatgcta ttccccaaagg tttcgaagac
 601 gccgtggagt tgcgcaggaa gaatcgag acgtggtca agtataatgaa caccaaaggc
 661 caggatcgcc tgcgccgcca tgaactttc gtgcaggacg gctgtggcgg tttatggacc
 721 accgataccg gctcgcccat cgtcattcg tggcaaggaca agctggccga gcacgcggtg
 781 tggtcgctga aatgctccc ggattggag tggtaacaaca tcaaggctt cgagaccgac
 841 gatcccacc acttctgggt cgagtgcgac ggccacggca agatcctt cccgggtat
 901 cccgagggtt actacgagaa ccacttcctg cattcctcg agctggacga cggcaagatc
 961 aagcgcaacc gcgaattcat gaacgtttc cagaattgc gcgcctgag cattccggtc
 1021 ccgcagatca aacgcgaagg cattcccacc tgaggccatc ctggaagggg tgaactatgg
 1081 acgatctatt gcaacgcgta cggcgctgca aagcgctgca gcaacccgaa tggggcgatc
 1141 cgtcgccct gcgcgacgtg cagggcgtacc tgcgcggcag tccggcgctg atccgcgccc
 1201 gcgcacatctt ggcctgcgc gcgcacccctgg ccgggtcgcc cgcggcgagg cgctggtggt
 1261 gcagtgcggc gactgcgcgg aggacatgga cgaccacca

Fig. 16B

3E8 phzA SEQ ID NO:116

1	MREYQLKGF	TDNLELRRRG	SAVRVRRKRP	AIHGMAGZRL	RRLLERSFPP
51	AGFPRCPFRH	CAVLLSGTL	VQLSGRLANR	PKNRTESMPH	TCNFZGVMAI
101	AKKRLZVCPL	SNLVTTGFQA	KHSVMAIRHZ	LKLWRRSEAG	NFCPEKVSRRQ
151	FFRPVIPMSS	FQYGCQSIRT	GGDSHHARVP	TVERFTDNLE	LRRRN RATVE
201	HYMRMKGAER	LQRHSLFVED	GCAGNWTTES	GEPLVFRGHE	SLRRLAEWLE
251	RCFPDWWEHNN	VRIFETEDPN	HLWVECDGRG	KALVPGYPQG	YCENHYIHSF
301	ELENGRIKRN	REFTNPMQKL	RALGIAVPQI	KRDGIP TZLM	IIPIQEEIZR
351	CSIMLFPKVS	KTPWSCAGRI	ARRWSSIZTP	KARIACAAMN	FSSRTAVAVY
401	GPIPIPARPSS	FVARTSWPST	RCGRZNAFPD	WEWYNIK	

Fig. 17

He had a very good time, and when he got home he told his wife all about it.

3E8 phzB SEQ ID NO:117

1 MLDNAIPQGF EDAVELRRKN RETVVKYMNT KGQDRLRRHE LFVEDGCGGL
51 WTTDTGSPIV IRGKDKLAEH AVWSLKCLPG LGVVQHQG

Fig. 18A

3E8 PHZA SEQ ID NO:161

MREYQRLKGFTDNLELRRRN RATVEHYMRMKGAERLQRHSLFVE
DGCAGNWTTESGEPLVFRGHESLRRLAEWLERCFPDWEWHNVRIFETEDPNHLWVECD
GRGKALVPGYPQGYCENHYIHSFELENGRIKRNREFTNPMQKLRALGIAVPQIKRDGIPT

Fig. 18B

PhzB SEQ ID NO:162

MLDNAIPQGFEDAVELRRKN RETVVKYMNT KGQDRLRRHE LFVEDGCGGL WTTDTGSPIV IRGKDKLAEH AVWSLKCF
PDWEWYNIKV FETDDPNHFV ECDGHGKIL FPGYPEGYYENHFLHSFELDDGKIKRNREFMNVFQQLRALSI PVPQIK
REGIPT

Fig. 18C

PhzC SEQ ID NO:163

MDDLLQRVRRC EALQQPEWGDP SRLRDVQAYLRGSPALIRAGDILALRATLAGSPAARRWWCSAATAPRTWTTT

Fig. 18D

PA14 phzR SEQ ID NO:164

phzR DNA sequence : 1161 bp

CGTCGACGAGGCCGC CATGGCCAAGGTTGTGT CGGGAGGCgCTCCGACGACGATG
GAGCGTGCAGAGAACAAATGAGAAAGACGCCGTGAGGCCATCGGAGAGCCGTTCTAC
GGTTTCCGCAAAGATCCGGGGCGCGTCCCTCCAGCa CAGCGCAGTTCTGCGCGGCGC
CTCGTGTCCGTGCTCATCGAGAAGTTCTTCAAGCTCGTTCTGCGTGCCTGGCGGGC
GGCGAATGGGCTCGACCTCGTCCGGAACACCCGCACAGGGCCGTGGCGATATGTACTTC
CAGGTCCGGCTTGATAAAGGGAATTGTATGAGTGGATAAGACGGAAACAAAAAAGAATA
AAAACGCTGAAGAACGAATCTGCCGGATCGATTGTTGACTGGTGAAGCTGGCATGCA
TGATGAGAGAGAGGGATATCTCGAGATTTGTCAAGAATAACAACCGAGGAAGAGTTCTT
CTCCCTGGTCTCGAGATATGCGGTAATTATGGATTGAAATTCTTCAATTCCGGTGC
GGCGCCTTCCCGCTGACCGCCTAAATATCATTCTGTCATTACCCAGGGAAATG
GAAAGCAGATATATCTCGAAGACTACACATCCATCGACCCGATCGTGCCTGG
CCTGGAATACACCCGCTGATCTGGAATGGCGAAGACTTCCAGGAGAACCGTTCTG
GGAGGAAGCGCTGCATCACGGCATCCGTACGGCTGGTCATCCGGTCCGGCAAGTA
CGGGCTGATCAGCATGCTGTCCTGGTGCCTGGTCAGCGAGAGCATGCCGCTACGGAAAT
CCTGGAGAAGGAATCCTCCTGCTCTGGATCACCAGCATGCTGCAGGCTACCTCGGCGA
CTGCTGGCGCCGCGATCGTCCCGAAAGCAATGTGCGCCTGACCGCCAGGGAAACCGA
GATGCTCAAGTGGACCGCGGTGGCAAGACCTACGGCAGATGGCCTGATCCTGTCAT
CGACCAAGCGCACGGTGAATTCCATATCGTAATGCGATGCGCAAGCTCAACTCCAGCAA
CAAGGCGGAGGCCACCATGAAGGCCTACGCCATCGGCCTGCTCAACTGAATCGACGCCTC
GTCGCCTAGCGAGGCCGCCGC

Fig. 18E

PA14 PhzR SEQ ID NO:165

PhzR peptide sequence

MHDEREGYLEILSRITTEEEFFSLVLEICGNYGFEFFSGARAPFPLTAPKYHFLSNYPG
EWKSRYISEDYSIDPIVRHGLLEYTPLIWNGEDFQENRFFWEALHHGIRHGW
KYGLISMLSLVRSSESIAATEILEKESFLLWITSMLQATFGDLLAPRIVPESNV
RLTARE
TEMLKWTAVGKTYGEIGLILSIDQRTVKFHIVNAMRKLNSNKAEATMKAYAIGLLNZ

Fig. 18F

109/133

34H4 SEQ ID NO:118

1 ACCAACATCC TGGTCCTGAG CAACAGCCAG CGCCACGGCC TGGCCGCCGC
51 CTGGCCGATC GTGCTCGGCG CCTGCGCGGC GGTGGCGGCG CTGATCCTGC
101 TGCTCGGGCT CGGCCTGGGC GAGCTGCTGC GGCGCCACCC GTTGCTCCAG
151 CAGGGGCTCG CCTGGCTTGG CGTCGGCTGG CTCAGCTACC TGGCCTGGAG
201 CCTGTTCCGC AGCGCG

Fig. 19

33C7 SEQ ID NO:119

1 CCACCGAAGT AACGGGTCA GCTCGTCAC AACAGGCGTC GCTCCTCGGC
51 CTGCATCAGG CTGCCCAGCG GGCCCTGGAA CCAGTCGCGC GCGCCCGGTT
101 GAT

Fig. 20

25a12.3 SEQ ID NO:120

1 GCGGTGCCCT GGATGTGTC GTTGAAGCAG CACAGCTCGT CCTTGTAGCG
51 CTCCAGCAAC GGCAATGGCAT TGGTCTGGGC GAAGTCCCTG AATTGCAGCA
101 GGACCTTGGG CCACGGCGCT TGATCGCCTG GATGAACAGG TCGACAA

Fig. 21

8C12 SEQ ID NO:121

1 TATTGTGTA TAAGNCTCAG GcTCTGGAGG GGCGCTGGG CAGGCNNAAAC
51 NNCCTCGCGT NCTNGGCAC GANTTNCNA TGCTTCGNT GCTGCCGGCG
101 TCTCNCCTT CNGTACTAgT CTACGCGTGG ACAACGTGGC

Fig. 22

2A8 SEQ ID NO:122

1 NATTTGTGTA TAAGAGTCAG GATCGAACGC TTCTCTTCGC CGCAGGAAAG
51 CCACCGCCGA GCTGCTGAAG ATGCTCGAGC GCAAGGGACA AGATCATGGG
101 CTTGGGGCAT NCCNTCTNNA TCGATTCTN CCCACGCAAC GAAgTGATCA
151 AGGGTTGGTC GAAGCAGCTC GCCGACgAGG TCGGCGACAA GGTCCCTGTT
201 GCGGTTCCG AGGCCATCGA CAAGACCATG TGGGAGCAGA AGAACTGTT
251 CCCAACGCCG ACTTCTACCA CGCCTCGGCG TCNCCNTCC NGTGCTTCCA
301 CCTT

Fig. 23

41A5 SEQ ID NO:123

1 tcgttgtaca ggccgaacag gccgagctgc caggtgtcgc cctcg

Fig. 24A

50E12 SEQ ID NO: 124

```
 1 gagcagacct gggtacccat ggttccttg acccgctgca cgatgtatgcc cagccgc  
61 ttcagatcct tggcgagtt ctttcttg acgatttgc gcagcgtgtt gagcatgtc  
121 gggccttgt ctccgtttc agtcccgcgc cagaaggcgc ggggccagtt cttcaggc  
181 gcggcggtag acctcgct tgaaggtcac cacctgtccc aggggttacc agtaactcac  
241 ccagcgccag ccgtcaact cgggcttgc ggtgatatcc atgcgcacgc ggcctcg  
301 ggacatcagc cgcaagcagga accatttctg cttctggccg atgcacagcg gctggctgtg  
361 ggtccgcacc aggcgcgtcg gcaaacggta gcgcagccag ccgcgg
```

Fig. 24B

35A9 SEQ ID NO: 125

```
 1 cgcgacagta gcatataatc aatcätgagt gattaattaa ttggcgtttc tgtaacatat
 61 ccttatgatc tgcggcgct ttcccttgtg aggacgttca gtggccagga aaaccaaaga
121 ggaatcccag aaaaccgcg acggcatact cgatgccgcc gagcgggttt tcctgaaaa
181 qqqcgtqqqc accactqcca
```

Fig. 24C

pho23 SEQ ID NO: 126

1 tcgatccaa tgactacaag gacgaaatcc gccagatgc cccgcacaag gccaacctgg
61 agctggacct gaagggcgac atcggctgga gcctgttccc ctggctggc ctggagc

Fig. 24D

6G12 SEQ ID NO: 127

```
1 ggatagggtgc ggcggaaaac gtacgggacg aaagagcggt ttcccgaat gacgcaccc  
61 cctgcaagcg caacttgcgt gttgtcgata gcaagtaagg cgcgagacat gtcctgaact  
121 tcatggggc tttttcttata agggcggact gtcgattctg ctagctggta atcctcttt  
181 tattgtctct gtgtgcgtt ttgttatgga tgtgtcgaat atttgaata tcgcccgtca  
241 actttatcca gggccgcagt tcagtgatt atttctcga aaagttgtt tttccaata  
301 ttcatqcttc ataqtctqqc cqccc
```

Fig. 24E

25F1 SEQ ID NO: 128

```
1 gcaggaaacc gtttccana tcctggcga gaatccctgg cacatgcacg ccggctccgg
61 cgagcagtcc ggcgacattg acgaacggtc ggcagtc ttc ctggggcggc ggcgcgtcca
121 tcaccaccag gtcgcgtcc cctccctgcc agcggaaata acgacggaag ctggcgtcgc
181 tactggccgg gatcagttcg gcggggggca cttccccca accttcggca acgaacaact
241 cgggcaaaaca agagtccaaac cagcaattca gtcgtggaa acgggcatca tcagacattt
301 acggggttct ccacggccct agccgttgcq caqgtcatqc ttattatcc agcattttt
```

Fig. 24F

1/1 atg aac atc acc ctc atg gcc atc ctg ggc atg gcc atc ctg ttc ggc atg gcc gac gac tat acc gcc ggc aag gaa tac gtc gag ctg aac ggc aag gtc gag 91/31

1/1 atg aac atc acc ctc atg gcc atc ctg ggc atg gcc atc ctg ttc ggc atg gcc gac gac tat acc gcc ggc aag gaa tac gtc gag ctg aac ggc aag gtc gag 91/31
N R N L I L T A M L A S L P G W A Q A D Y T A G K E Y V E L S S P V P V

121/41 tcc cag ccc aag atc gaa gtg gtc gaa ctg ttc tgg bat ggc tgc ccg cat tgc tac ggg ttc gag ctg acc atc gtt cgg acc atc gtt cgg aag ctg cga gat gtc cat ttc gtc 151/51
S Q P G K I E V V E L F W Y G C P H C Y A F P T I V P H S E K L P A D V H F V

241/81 cgc ctg cct gcc ctg ttc ggc ggt atc tgg aac gtc cat ggg cag atg ggt gtc gag cat gac gtc cac aac gtc cac atc cac aag gag 271/91
R L P A L F G I W N V H G Q M F L T L F S M G V H D V H N A V F E A I H K F
361/121 ccc aag atc ctc gcc act ccg gaa gag atg ggc gat ttc ctc gcc ggc aag ggc gtc gag aag gaa aaa ttc ctg aac acc tat aat tcc ttc ggc atc aag ggc gag atg gaa aag gcc 391/131
H K L A T P E E M A D F L A G K P L S T Y N S F A I K G Q W E K A

481/161 aag aag ctg ggg atg gcc tac cag gtc acc ggc gta cgg acc atg gtt gtc aat ggc aac ttc ggc tcc gac atc ggc tcc gac aac ttc ggc aag ctg gac tac 511/171
K K L A M A Y Q V T G V P T M V V N G K Y R F D I G S A G G P E E T L K L A D V

601/201 ctg atc gag aaa gag cgg ccc aag aag tag 631/211
L I E K R A A K K *

Fig. 24G

Sequences of PA14 50E12 encoding for YgdPPa and PtsPPa

1/1 31/11 61/21 91/31
 GAA AAG GCC CAG ACG CAC GGG GTG ACT CCA TCG GTT GGC GGG TGG CGG gAG GGC CCC GAG ACC CTT TTG CGA AGG CTC CCA CGG GGC CTT GGG AAA aCC CCT AGC CTA CGG GCT TTT GGC
 121/41 151/51 181/61 211/71
 GGC CCT GTA TCC TCC CGG CAC GAG TCG CAA AGC CGC GGG TTG CGG CTA TCA CAA GCT TTA TGG AAC AAT GCG GGC ACA TCC GAT TTC GAG GAT GTC CCA CGG TGA TCC ATT CCG ATG GTT
 M I D S D G F
 241/81 271/91 301/101 331/111
 TTC GCC CGA ATG TCG GCA TCA TCC TCG CCA AGC AGG CGG GGC AGG TGC TGT GGG CGC GGC GTA TCA ATC AGG AAG CCT GGC ACT CCT CGC AGG GAG GCA TCA ATG ATC GCG AAA CGC CGG
 R P N V G I I L A N B A G Q V L W A R R I N Q E A W Q F P P Q G G I N D R E T P E
 361/121 391/131 421/141 451/151
 AMG AGG CGC TGT ATC GCG AAT TGA AGC AAG TCG GGC TGG AGG CGG AGC TGC GCA TCC TGG CCT GCA CGG CGC GGT GGC TGC GCT ACC GTC CGC AGC GGC TGG TGC GGA CGC
 E A L Y R E L N E B V G L E A G D V R I L A C T R G W L R Y R L P Q R L V R T H
 481/161 511/171 541/181 571/191
 ACA GCC AGC CGC TGT GCA TCG GCC AGA AGC AGA AAT GGT TCC TGC TGC GGC TGA TGT CGG AGC AGG CGC GGC TGC GCA TGG ATA TCA CCA GCA AGC CGC AGT TCG AGC GcT GGC GCT GGG
 S Q P L C I G Q X Q X W F L L R L M S D E A R V R M D I T S K P E F D G W R W V
 601/201 631/211 661/221 691/231
 TGA GTT ACT GGT ACC CCC TGG GAC AGG TGG TGA CCT TCA AGC CGC AGG TCT ACC GGC GGG CCC TGA AGG AAC TGG CGC CGC GGC TTC TGG CGC GGG ACT GAA CAC GGA GAC AAG GGC CGG
 S Y W Y P L G Q V V T F K R E V Y R R A L K E L A P R L L A R D *

721/241 751/251 781/261 811/271
 AGC ATG CTC AAC ACG CTG CGC AGG ATC GTC CAG GAA GTC AAC TCC CGC AGG GAT CTG AGG CGG CGC CTG CGC ATC ATC GTG CGG CGC GTC AAC GAA GGC ATG GGT ACC CAG GTC TGC TGG
 M L N T L R K I V Q E V N S A K D L K A A L G I I V Q R V K E A M G T Q V C S

841/281 871/291 901/301 931/311
 GTG TAC CTG CTC GAC AGC GAG ACC CAG CGT TTC GTC CTG ATG GCT ACT GAA GGC CTC AAC AGG GCT TCC ATC GGC AGG GTC AGC ATG GGC CCC AGC GAA GGC CTG GTC GGC CTG GTC GGC
 V Y L L D T E T Q R F V L M A T E G L N K R S I G K V S M A P S E G L V G L V G

961/321 991/331 1021/341 1051/351
 ACC CGC GAG GAG CGG CTC AAC CTG GAG AAC GCC CCC CGC CGC TAC CGC TAT TTC GGC GAG ACC GGC GAG GAG CGC TAC GGC TCG TTC CTC GGC GGG CGC ATC ATC CAC CAT acc
 T R E E P L N L E N A A A H P R Y R Y F A E T G E E R Y A S F L G A P I I H H R

1081/361 1111/371 1141/381 1171/391
 CGG GTG ATG GGG GTG CTG CTG CTG CAG CAG AGG GAG CGC CGC CAG TTC GAC GAA GGC GAG Gag GGC CTC CTC GTC ACC ATG AGC GGC CAG CTC GGC GGG GTC ATC GCG CAT GGC GAG GGC
 R V M G V L V V Q Q X E R R Q F D E G E B A F L V T M S A Q L A G V I A H A E A

1201/401 1231/411 1261/421 1291/431
 ACC GGT TCG ATC CGC CGC CTG GGC AAG CTC GGC AGG GGC ATC CAG GAA GGC AAG TTC GTC GGC GTG CCC GGC CCC GGG GTC GGC AGG GGC GTG GTG TTG CCT CGG GGC
 T G S I R G L G X L G K G I Q E A K F V G V P G A P G V G V G K A V V V L P P A

1321/441 1351/451 1381/461 1411/471
 GAC CTG GAA GTG GTG CGG GAC AAG CAG CAG GTC GAC GAC GAC ATC GAC CCC CTG TTC AAC CAG GAG CGC CTG GAG GGC GTT CGC GGC GAC ATG GGC CGC CTG TCG AGC AAG CTC GGC AGC
 D L E V V P D K Q V D D I D A E I A L F X Q A L E G V R A D M R A L S S K L A S

1441/481 1471/491 1501/501 1531/511
 CAG CTG CGC AAG GAA GAA CGC CGC CTG TTC GAC GTC TAC CTG ATG ATG CTC GAC GAT GTC GAT GGC TCC ATC GGC AAC GAG GTC AAG CGC ATC ATC GTC ACC GGC CAG GGC GGC CGC CTG
 Q L R K E E R A L F D V Y L M M L D D A S I G N E V K R I I R T G Q W A Q G A L

1561/521 1591/531 1621/541 1651/551
 CGC CAG GTG ATG GAG CAC CTG CAG CGC CGC TTC GTC CTG ATG GAC GAC GAC GGC TAT CTC CGC GAG CGC CGC TCC GAC GTC AAG GAC ATC GGT CGC CGC CTG CTC GGC TAC Ctg CAG GAA Gha
 R Q V V V M E H V Q R F B L M D D A Y L R E R A S D V K D I G R R L L A Y L Q E E

1681/561 1711/571 1741/581 1771/591
 CGC AAG CAG AAC CTG ACC TAC CGG GAG CAG ACC ATC ATC GTC AGC GAG GAG GAG CTG TCG CGG CGC ATG CTC GGC GAG GTC CGG GAG GAA GGG CGC CTG GTC GTC TCG CTG GGC TGC
 R K Q N L T Y P E Q T I I V S E E L S P A M L G S V P E G R L V G L V S V L G S

1801/601 1831/611 1861/621 1891/631
 GGC AAC TCG CAC GTG CGG ATC CTC CGC CGC CGT CGC ATG GGC ATC CCC AGC CGC ATG GGG CGC CGC GAC CTG CGC TAC TCC AAC GTC GAC GGC ATC GAC CTG ATC GTC GAT GGC TAC CAC CGC
 G N S E V A I L A R A M G I P T V H G A V D L P Y S K V D G I D L I V D G Y H G

1921/641	1951/651	1981/661	2011/671
GAG GTC TAC ACC AAC CCC TCC GCC GAG CTG GTG CGC CAG TAC AGC GAC GTG GTC GCC GAG CGC CAG CTG AGC AAG GGC CTG GCG GGC CTG CGC GAG CTG CCC TGC GAG ACC CTC CTC GAC E V Y T N P S A E L V R Q Y S D V V A E E R E L S K G L A A L R E L P C E T L D			
2041/681	2071/691	2101/701	2131/711
GGC CAC CGC ATG CGG CTC TGG GTC AAC ACC GGC CTG CTC GCC GAT GTC GCC CGC GGC CAG GAG CGT GGC GCG GGC GAG GGC GTG GGC CTG TAC CGC ACC GAA GTG CGC TTC ATG ATC AAC GAC G H R M P L W V N T G L L A D V A R A Q E R G A E G V G L Y R T E V P F M I N D			
2161/721	2191/731	2221/741	2251/751
GCG TTC CCC AGC GAG AAG GAA CAG CTG GCG ATC TAC CGC GAG CAG CTC AGT GCC TTC CAC CGG CTG CGG GTG ACC ATG CGC ACC CTG GAT ATC GGC GGC GAC AAG GCG CTG TCC TAC TCC R F P S E K E Q L A I Y R E Q L S A P H P L P V T M R T L D I G G D K A L S Y P			
2281/761	2311/771	2341/781	2371/791
CGC ATC AAG GAA GAC AAC CGG TTC CTC GGC TGG CGC GGC ATC CGC GTC ACC CTC GAC CAC CGG GAG ATC TTC CTG GTC CAG ACC CGC GGC ATG CTC AAC AGC GAC GAA GGA CTG GAC AAC P I K E D N P F L G W R G I R V T L D H P E I F L V Q T R A M L K A S E G L D N			
2401/801	2431/811	2461/821	2491/831
CTG CGC ATC CTG CTG CGG ATG ATC TCC GGC ACC AAC CAC GAG CTG GAA GAG GGC CTG CAC CTG ATC CAC CGC GGC TGG GGC GAG GTG CGC GAC AAC GTC GGC ATC GGC ATC CGC CCT ATC L R I L L P M I S G T E E L E E A L H L I H R A W G E V R D E G V D I A M P P I			
2521/841	2551/851	2581/861	2611/871
GGC ATG ATG GTC GAG ATT CGC GGC GTG TAC CAG ACC CGC GAG CTG GGC CGT CAG GTC GAC TTC CTT TCG GTC GGT TCG AAC GAC GTC CTG ACC CAG TAC CTG CTG GCG GTC GAC CGC AAC G M M V E I P A A V Y Q T R E L A R Q V D F L S V G S N D L T Q Y L L A V D R N			
2641/881	2671/891	2701/901	2731/911
ATT CGG CGG GTC GCC GAC CTC TAC GAC TAC CTG CAT CGG GGC GTG CTG CAT CGG TTG AAG AAG GTG GTC GAC GAT GGC CAC CTG GAA GGC AAG CGG GTG AGC ATC TGC GGC GAG ATG GGC N P R V A D L Y D Y L H P A V L H A L K X V V D D A H L E G K P V S I C G E M A			
2761/921	2791/931	2821/941	2851/951
GGC GAT CCC GGG GCT GCC GTG CTG CTG ATG GGC ATG GGC TTC GAC ACC CTG TCG ATG AAC GCC ACC AAC CTG CCC AAG GTG AAG TGG CTG CTG CGC CAG ATC ACC CTG GAC AAC GGC CGG G D P A A A V L L M A M G F D S L S M N A T N L P K V K W L L R Q I T L D K A R			
2881/961	2911/971	2941/981	2971/991
GAC CTG CTC GCC CAG TTG CTC ACC TTC GAC AAC CGG CAG GTC ATC CAC ACC TCG CTG CAC CTG GCG TTG CGC AAC CTC GGC CTG GGT CGC GTG ATC AAC ACC CGG GCT ACC GTC CAG CGC D L L G Q L L T F D N P Q V I H S S L H L A L R N L G L G R V I N P A A T V Q P			
3001/1001			
TGA TTT TCC C			
*			

Fig. 241

Sequence of PA14 35A9 encoding mtrRPa

1/1 31/11 61/21 91/31
 GTC GAT TTG GAA CAG CAC GGT GCC GGC GAC Tgc CTG GCC TTC CTC GTA CAG GCG AGC GGT GAC GAT GCC GGC GAC GCG CGC CGC CTC gGC CTG GCG GTA CGC TTC CAG GCG TCC

121/41 151/51 181/61 211/71
 GGG CAG CTC GCT GGT GAT GCC GAT gGG CGC CGG CCT GGC GAC GAT CAC GGC GAC CTC GGC GGG GGC CTC CGC AGT CTT CCC GGT GTC CGC TGC TTC GCA GGC CAG CAG GAA TAG GGC

241/81 271/91 301/101 331/111
 GAC CAG GGC CGC CAG CAG CCC GCG CAG CGA GCC GGT CCA TTG GAT GTG CAT GGG TGT CCC TCG ATT CGT GAA CTC GCG AGC TTG CCC GGG AAG GGG CAC CGC AAC TCA CGA CGG CGA

361/121 391/131 421/141 451/151
 CAG TAG CAT ATA ATC ATAT CAT GAG TGA CTA ATT ATG TGG CGT TTC TGT AAC ATA TCC TTA TGA TCT GCG GCG CCT TTC CCT TGT GAG GAC GTT CAG TGG CGA GAA AAA CCA AAG AGG AAT
 M A R K T K E B S

481/161 511/171 541/181 571/191
 CCC AGA AAA CCC GCG AAG GCA TAC TCG ATG CGG CGG AGC GGG TTT TCC TGG AAA AGG GCG TGG GCA CGA CTG CGA TGG CGG ACC TGG CGG AGC CGG CGG GGG TTT CTC GCG GTG CGG TCT
 Q K T R D G I L D A A B R V F L E K G V G T T A M A D L A D A A G V S R G A V Y

601/201 631/211 661/221 691/231
 ACG GCC ACT ACA AGA ACA AGA TCG AGG TCT Gtc TGG CGA TGT GCG ACC CGC CCT TCG GCG AGA TCG AGG TAC CGG AAG AAA AGG CGA GGG TGC CGG CGC TGG Aca TCC TCC TGC GCG CGG
 G H Y K N K I E V C L A M C D R A F G Q I E V P D E N A R V P A L D I L L R A G

721/241 751/251 781/261 811/271
 GCA TGG GCT TTC TCC GGC AGT GCT GCG AaC CGG GTT CGG TGC AGC GGG TGG AGA TCC TCT ACC TCA AGT GCG AAC GCA GCG AGC AGA AGC CGC TGT TGC GGC GGC GGC AGC TGC
 M G F L R Q C C B P G S V Q R V L E I L Y L K C E R S D E N E P L L R R R B L L

841/281 871/291 901/301 931/311
 TCG AGA AGC AGG GGC AAC GCT TCG GGC gac GGC AGA TCC CGC GGG CGG TGG AGC GGC GGG AAC TGC CGG CGC GGC TGG AGC TCG AGC TGG CGA TCT ATC TGC AAT CGC Tgt GGG AGC
 B K Q G Q R F G R R Q I R R A V E R G B L P A R L D V E L A S I Y L Q S L W D G

961/321 991/331 1021/341 1051/351
 GCA TCT GCG GCA CGC TCG CCT GCA CGG AGC GCT TGC CGC AGC ATC CCT GGA gCC GGG CGG CGC AGC GCA TGT TCC CGC CGG CGC TCG AaA GGC TGC GCA GTI CTC CCT ACC TCT TCC TGG CGG
 I C G T L A W T E R L R D D P W S R A E R M F R A G L D S L R S S P Y L L L A D

1081/361 1111/371 1141/381 1171/391
 ACG CCT GAG GGC GTC AAT CGT CGG CGA CCA TCA GGT GCC TGC GCT GGT CCT CGG CGC CGG CGA CGA CGA CGC CGC GCT GGG CGT Cct CCT CGC TGA TGT GCA GGC GCT TGC Cat CGA TGT AGA GCA
 A *

1201/401 1231/411 1261/421 1291/431
 CGG ACA GGC GGC CCT CGG CGT CGG TAC CGA TGC GCA GGC TGT CGA CGG CGG CGC GAT GCC GGC TGC CTT CGA TCT CGA CGC TGC AGA tGC CTT CGG AAT CGA TTT CGA TGG ACA TGG

1321/441 1351/451 1381/461 1411/471
 GAA CCT CGC GTT Ttc TCC GGC TAC CCT GGG TGG ACC CGC GGC ATC CGC GCG GGT TCT GTC AGC GTA GCT TCA CGC CAG CGT CAC CGG CCT CGC ACC CGG CTT CGC TGC AAT CGT CGG CGA

1441/481 1471/491 1501/501
 AGA aGG CGA CGC CAG CGG AGG AGC AGC CGA CGC TGC GGC TAT CGG TGA TTG GTG CGG GGT AAG TGG GAC TGC TGA

Fig. 24J

Sequences of PA14 25F1 encoding for *orfT*, *OrfU* and *DjIApA*

31/11	61/21	91/31
CGA GGA ATC CAG TCG AGG TGC Gag TAG TCC GCA CTG CGG GAT CTC AGC GCG CGA CCA CGG GAC TCG GTG ACC AGG CCG TGG GTC TCT GCC TCG AGC GTT TCG CCT CGG CTG CGG GAC		
121/41	151/51	181/61
ACG CTG CTG CCC GCG GCG GCG GTG CTG ACC GAG GTC GCG GTA TGC GCG GGG CGC GGT GCG AGG TTG GCA TTG GCG TTC TGC AGC AGG GAG CAA TCC CAG CGG CGG GTG GCG GAT ACC TTG		211/71
241/81	271/91	301/101
CAG TCG AAC TGA TCG GCG GCC TGT ACA GTC AAT GCT GCG ACC GGC TGC AGA GCC AGC AGG CTG CGG GTG ACC AGC AGG GGA AAC TTT CTT CGA AAC AGC AGG GAT TTC ACT GCC ATC TTG		331/111
361/121	391/131	421/141
TTA ATC CGG GCT TCC TGC GCG CCA TCG CGG TGG GCG GCA CGC CTC TCG ATG GGC TGA AAA AGA TCC TGG ATA ATA AAG CAT GAC CTG CGC AAC GGC TAG GGC CGT GGA GAA CCC CGT		451/151
481/161	511/171	541/181
AAA TGT CTG ATG ATG CCC GTT TCC AGC AGC TGA ATC GCT GGT TGG ACT CTT GTT TGC CGG AGT TGT TCG TTG CCG AAG GTT GGG GGG AAG TGC CCC CGG CGG AAC TGA TCC CGG CGA GTA		571/191
M S D D A R P Q Q L N R W L D S C L P E L F V A E G W G E V P P A B L I P A S S		
601/201	631/211	661/221
GGG AGC CCA GCT TCC GTC GTT ATT TCC GCT GGC AGG GAG GGG ACC GCA GCG TGG TCG TGA TCG AGC CGC CGC CGC CCC AGG AAG ACT GCC GAC CGT TCG TCA AGG TCG CGG GAC TCG TCG		691/231
D A S F R R Y F R W Q G G D R S L V V M D A P P P Q E D C R P F V K V A G L L A		
721/241	751/251	781/261
CGG GAG CGG GCG TGC ATG TGC GGA GGA TTC TCG CCC AGG ATC TGG AGA AGC GTT TCC TGC TGC TCA GTG ACC TGG GCC GGC AGA CCT ACC TCG AGC TGC TTC ATC CGG GAA ATG CGG AGC		811/271
G A G V H V P R I L A Q D L E N G F L L L S D L G R Q T Y L D V L H P G N A D E		
841/281	871/291	901/301
AGC TGT TCG AAC CGG CCC TGG ATG CGC TGA TCG CCT TCC AGA AGG TCG ATG TCG CGG GTG TCC TGC CTG CCT AGC AGC AAG CGG TGC TGC TGC GCG GCG AGC TGC AGC TGT TCC CGG ACT GGT		931/311
L F E P A L D A L I A F Q K V D V A G V L P A Y D E A V L R R E L Q L F P D W Y		
961/321	991/331	1021/341
ACG TGG CCC GCC ACC TCG GCG TGG AGG AGG CGC AGC CGG TGG CCC GCT GGC AGC GGA TCT GCG ACC TGC TGG TAC GCA GGG CGC CGC TGG AGC AAC CGC GGG TGT TCG TCC ATC CGC ACT		1051/351
L A R H L G V E L E G E T T L A R W Q R I C D L L V R S A L E Q P R V F V H R D Y		
1081/361	1111/371	1141/381
ATA TGC CGC GCA Acc TGA TGC TCA GCG AGC CCA ACC CGG CGC TCC TCG ACT TCC AGG AGG CGC CCC TGC AGC AGG TCA CCT AGC ATG TCA CCT CCT GCC TGT ACA AGG ATG CCT TCG TCA GTT		1171/391
M P R N L M L S E P N P G V L D F Q D A L H G P V T Y D V T C L Y K D A F V S W		
1201/401	1231/411	1261/421
GCG CGG AGC CGC GCG TGC ATG CGG CGC TGA GTC GTT ACT GGA AGA AGG CGA CCT GGG CGG GCA TCC CGC TGC CGC CAA GCT TCG AGG ACT TCC TCC GCG CCA CGG ACC TGA TGG CGG CGC		1291/431
P E P R V H A A L S R Y W K K A T W A G I P L P P S F E D F L R A S D L M G V Q		
1321/441	1351/451	1381/461
AGC GCC ACC TGA AGG TGA TTG GCA TCT TCG CCC GTA TTT GTC ACC CGG AGC GCA AGC CGC GCT ACC TGG GTG AGC TGC TGC CAC GCT TCT TCC GTT ATC TGG AAA CGG CGG TGG CGC GCC GTC		1411/471
R H L K V I G I F A R I C H R D G K P R Y L G D V P R F F R Y L E T A V A R R P		
1441/481	1471/491	1501/501
CCG AGC TGG CGG AAC TGG CGG AGC TGC TGG CCT CGC TGC CGC AGG GAG GAG CGG AGG CAT GAA GGC GAT GAT CCT CGC CGC CGG CGG TGG CGA CGG CAT CGG GAC CAC CCT GCA CAC CGC		1531/511
M K A M I L A A G R G E R M R P T T L H T P E L A E L G E L L A S L P Q G A E A		
1561/521	1591/531	1621/541
CAA GGC GCT GAT CGA GGC GGC CGC CGG CGT GCC ATT GAT CGA GGC GCG TCA GTT GCT GCG GCT GCG CCA GGC CGG AGT CGA CGA CGA CTG GTG GAT CAA CCA CCA TGC CTG GCT TGG CGA GCA GAT CGA GGC		1651/551
K P L I R A A G V P L I E R Q O L L A L R Q A G V D D W V I N H A W L G E Q I E A		

Fig. 24K

116/133

1681/561	1711/571	1741/581	1771/591
CTA TCT CGG CGA CGG CTC GCG CCT CGG CGG CGG GAT CGC CTA TTC aCC cGA ACC GCT GGA AAC CGG CGG CGG TGG AAT CTT CCG CGG CCT GCC GTT GCT CGG CGA GCA GGC GTT CCT Y L G D G S R L G G R I A Y S P E G E P L B T G G G I F R A L P L L G E Q P F L			
1801/601	1831/611	1861/621	1891/631
GTT GCT CAA CGG CGA TGT CTG GAG CGA CTT CGA CTA CTC TCG GCT GCA TCT TGC CGA CGG CGA CCT GGC GCA TCT GGT GCT GGT CGA CAA CCC GGC GCA CCA TCC CGC CGG CGA TTT CGA L L N G D V W S D F D Y S R L H L A D G D L A H L V L V D N P A H H P A G D F H			
1921/641	1951/651	1981/661	2011/671
CCT GGA TGC CGG CGG ACG GGT GGG CGA GAC CGG CGA AGC GGG CGG CGA CCT GAC CTA CAG CGG GAT CGC CGT ACT GCA TCC CGG GCT GTT CGA GGG CTG CCA CGC CGG CGC CTT CAA CGT L D A G G R V G E T R E A G G N L T Y S G I A V L H P A L F E G C Q P G A F K L			
2041/681	2071/691	2101/701	2131/711
GGC GCC GCT ATT GCG CAA CGG CAT CGC CGC GGG GCG GGT CAG CGG CGA ACA CTA TCG TGG GCA GTG GGT CGA CGT CGG TAC CGA CGA GGG CCT GGC CGA AGT CGA CGG ATT GCT CGC CGA A P L L R K A I A A G R V S G E H Y R G Q W V D V G T H E R L A E V E R L L A E			
2161/721	2191/731	2221/741	2251/751
GCA CGC CTG AGA TGC TCT CGC CGG CTA CGC TGA TCG GAG CGG CGG GCT GGG CGG CCC TGG CCA GCA TCC CGG CCC TGC TCG CGG CGC CGC TGC TGG CGC AAC TSC TCC ACC GCA GGT CGC H A * M L W P A T L I G A G A G W A L A S I P G A L L G G L L G Q L L D R R L R			
2281/761	2311/771	2341/781	2371/791
GCC TGG AGT CCT CGC CGG CGC TCC TGG CGC GTC GCG GGG CGG TGA AGC ATG AGG AGC ACC TGC TGT TCC AGT TGC TCG CGT ACT TGC CGA AGA CGC CGC CGG GGG TGG AGG AGA L E S W R G L L A R L R G R A V N D E D D L L F Q L L G Y L A K S G G R V E E M			
2401/801	2431/811	2461/821	2491/831
TGG ATA TCC CGC AGG CGC CGG AGG AGA TGG CGT TGC GCA AGC TCG ATA CGC GAG CCC AGC CGC GTG CCA TCG CGT CCT TCG GCA AGG CGA AGG CGG CGA TCG CCT ATT TGC AGG CGG AGG H I R Q A R E E M A L R K L D R R A Q R R A I A S F G K G K A G I A H L Q A E V			
2521/841	2551/851	2581/861	2611/871
TGG CGC GTC TGA AGG CGG AAC GTG CGG AGG CGG CAG TAT TGC TCG CCT GCT CGC GGA TGG CCT GGG CTG CGC CGG TCC TCA CGC AGT CGG CGG GAC AAC TGG TGT TCC ATT GGG CGC GCT CGC A R L K G E R A E A V L L A C W R M A W A G G G V L S Q S A R Q L V L Q W G R W L			
2641/881	2671/891	2701/901	2731/911
TGG GTT GGT CGG CGG AGC GAA CGG AAC GCT TGT CGG CGC GGG TCA TGC CGA AGC GGA CGC CGG CGC GTG CGT CGG CCC TGC TGC TCC TGG CGG TGG AGG CGG GAA G W S A E R T E R L S A R V M P K R T R A V A R D S Y R E A L L L G V E A G S			
2761/921	2791/931	2821/941	2851/951
CGG AGC CGG CGG CGC TGA TCA AAC CGG CCT ATC GCA AGC TGA TCA CGC AGC ATC ATC CGG ACA AAC TGG CGG GAG CGG CGG CGA CGC CGG TGC GTG CGG CGG CTA CGG AGA AAA CGG GTG B P A L I K R A Y R K L I S Q H H P D K L A G A G A S V E R V R A A T E K T R E			
2881/961	2911/971	2941/981	2971/991
ATT TGC AGG CGG CCT ATC CGG CCC TCG TCC GAG AGC GTG AGG GGT TCC GCT GAT CAC TCC GCA GGT TTC TGC TCC CGC TGC AGG TGA AGA CGT AGC CGG CGG ATT CGT CGG TAC AGT L Q A A Y A L V R E R E G F R *			
3001/1001	3031/1011	3061/1021	3091/1031
TGC TCC TGC TCC CGC TTG GGG TCG GGC GGT AGa GGC TGC ATC GCG ATT TGT AGC TAG AGC TGC CGC TTG CGC CGC CGC TGC ATG CGC AGC CGG CGG ATT CGT CGG TAC AGT TGC TCC TGC TCC CGC TTG GGG TCG GGC GGT AGa GGC TGC ATC GCG ATT TGT AGC TAG AGC TGC CGC TTG CGC CGC CGC TGC ATG CGC AGC CGG CGG ATT CGT CGG TAC AGT			

Fig. 24L

1 CTGCAGCGTC TGCCGACCT GCTGCAACTG ATCCCGGGAC ACGGCGGCCT
 51 GCTGCGGGGG CGGCTGGCCG CGGATGGGGC CGAGTCGGCC TATACCGAGT
 101 GTCTGCGCCT GTGCCGACGG TTGCTCTGGC GCCAGTCCAT GGGCGAGTCC
 151 CTCGACGAAC TGAGCGAGGA GCTGCACCGC GCCTGGGGAG GGCAGAGCGT
 201 CGACTTCCTG CCCGGCGAAC TGCACCTGGG GAGCATGCGC CGGATGCTGG
 251 AGATTCTCTC CCGCCAGGCG CTGCCTCTGG ACTGAGGCAG AACATCCATT
 301 GCGGCGATCG CGCCCGACGG CTGCGGTCGC AATTGGGGGA AATGGGGGTA
 351 TCGATGATGA ATATGCCGTT GCGCGCTAGC GTCGCGCAGG CCAGTCGCC
 401 ATGGGCGCGG GGAGGTGGCT CGTGAGTGGG GTTGGCTATC GACTGGAAGA
 451 AAGTCTGGAG TACCGCACGC TGTTGCCGGA GGCGCTGTCG ATCTGGCGCA
 501 TGGCTGGCGC CAACCGGATG CTGTTGACT GCTTCGACGT GGACAGCAAG
 551 GCTGCGCGC GTAGCGTGGC GATCCTTCC AGCTGCCTGC GCATCGAGTG
 601 CTGGGGCGC GATGTGGTGC TGCGGGCGTT GAACTCCAAC GGACGCGCCT
 651 TGCTGGCGCC GTTGAGCGAG GCCTGTCCGG CCCAGGTAC CGTCTTGCCTG
 701 GACGGCGACA CCCTGCACTG GCGCTTCCCC CCGGAAGAGC CGCATGCGGA
 751 CGAGTGGCGA CGCCTGCATG GCCTGTCCAG CCTGGAGGCG CTGCGCCGCG
 801 TGCTCGGAAC GCTGGGCGAC GCGGAGGGGC CTGCGCTGCT GGGCGGCCCTG
 851 TTCAGTTTCG ACCTGGCCGA GCAGTTCGAA CCCTTGCCGG CGCCGGCCGA
 901 ACCTGCGCGG CATTGCCCGG ACTACCTGTT CCTGGTGCCG GAGTTGCTGC
 951 TGGATATCGA TCACCTGGCG CGCCGGACTT CGCTGCAAGC GTTCGTCCAC
 1001 GATCCGGCCG GGCACGACCG GTTGGCCGCC AGCCTGCGCC AATGTGCCGA
 1051 CGAATTCCAT GGCGCCGTGG AGGAGGCTTC CGAGTCGCCG GTGGCAGGCG
 1101 TACGGGCCGG CAAACTACCAG GTCGACCTGG ACGATGCGAG CTTGCCCGC
 1151 CAGGTAGAAC GCCTGCAGGC CCACGTGAGG GCGGGCGACG TGGTCCAGAT
 1201 CGTACCTTCG CGCAGCTTCA GCATGCCGTG CGCGGACCCCC TGGCGGGCCT
 1251 ATGCCAGTT GTGCCTGCGC AACCCAGCC CGTACCGCTT CTCCTCGAT
 1301 GCGGGGGACT TCTGCCTGTT CGGCGCTTCG CGGGAGTCGG CATTGAAGTA
 1351 CGACCGGGAG AGTCGCGAGG TGGAACTCTA TCCCATTGCC GGCAACCGCC
 1401 CGCGCGGATG CGATGCCCGG GGGCCATCG ATGCGGAACG GGACAATCGC
 1451 CTGGAAGCGG AGTTGCGCCT GGATGCCAAG GAGATGCCG AGCACATGAT
 1501 GCTGGTCGAC CTGGCGCGCA ACGATCTGGC GCGCGTCTGC CGCAGCGGTA
 1551 CCCGGCAGGT GCGCGACATG CTCAAGGTGCG ATCGCTACAG CCACGTGATG
 1601 CACCTGGTCT CGCGCGTGGC TGGCGAACTG CACGGCGAAC TGGATGCGCT
 1651 GCATGCCCTAC CGTGCCTGCC TGAACATGGG CACCTGGTC GGCGCGCCGA
 1701 AGGTCCGTGC CATGCAGTTG CTGCGGCAGT ACGAGGATGG CTATCGCGGC
 1751 AGCTACGGTG GTGCGATCGG CATTCTCGAC AGCGCCGGCA ACCTCGATAC
 1801 CAGCATTGTC ATCCGCTCCG CCGAGGTCCG CGAAGGTATC GCGCGGGTTC
 1851 GGGCAGGCAGC CGGCGTGGTG CTGGATTGCG ATCCACGGCT GGAGGCGCAG
 1901 GAAACCCGCA ACAAGGGCCT GGCGGTGCTG ACCGCGGTGG CCGCTGCCGA
 1951 ACGCGAAAGG GGAGAGCGCG ATGCGCATCA CGCTGTTGGA TAACTTCGAT
 2001 TCCTTCACCT ACAACCTGGT CGAGCAGTTC TGCCTGCTCG GCGCGGAGGT
 2051 CGGGGTGATG CGCAACGATA CGCCGTTGCC GACGATCCAG GCGGCATTGC
 2101 TGGCCGACGG TTGCGAAGT CGGGTGTGT CGCCGGGGCC CGGTCGGCCG

Fig. 25A

2151 GAAGACGCCG GCTGTATGCT GGAATTGCTC GCCTGGGCC GCAGGGCGCTT
 2201 GCCGGTGTCTC GGCGTCTGCC TCGGCCACCA GGCGCTGGCG CTGGCCGCC
 2251 GTGGCGCGGT GGGCGAGGCG AGGAAGCCGC TGCATGGCAA GAGCACGTCC
 2301 CTGCGTTTCG ATCAGCGTCA CCCGCTGTTC GACGGCATCG CTGACCTGCG
 2351 CGTCGCGCGC TACCACTCGC TGGTGGTCAG TCGCCTGCCG GAAGGTTTCG
 2401 ACTGCCTGGC CGATGCCGAT GGCGAGATCA TGGCGATGGC CGATCCGCGC
 2451 AATCGACAGC TGGGCTTGCA ATTCCATCCC GAGTCGATTC TCACCACCCA
 2501 CGGCCAGCGT CTGCTGGAGA ACCGCTCTACT CTGGTGCAGGC GCGTTGGCGG
 2551 TCGCGGAGCG CCTTCGGGCC TGAGCGCGC TGCGCAGTTT CGACCGAGGC
 2601 TCGGGTGCCTA GGCCGGCGCA TCGTCGAAAC GCTGGCGGCC CAGTTCGCGC
 2651 AGGCGCTGGC GGGCGCTTTC GAGAAAGCGA CGGAAGCTGC GCTCGGATTG
 2701 CAGCGCGGTG TTGTAGTAGC AATACACCTT GGTGTCGATG CCGCCCGGTT
 2751 CGTACAGTTC GCTGAGGACT GCCAGGGTAC CGTTGCGCAG GCGTTCCCTcG
 2801 ACGAAATAAT GCGGCGAGAT GCCCCATCCG ACGCCGGCTT CCACCAGACG
 2851 CAGCATGTCG TCGAAGTTT CCACGAAGAG CACCTTGTGCTG CTGACCGGCC
 2901 GCAGCAGGTT CGAATGCTGC CCGGAGCGGC TgCCGAGGCT GATCTGCCGG
 2951 TAATTGGCCA GGCTCGCGAT GCTGTGCAGG GAGGCATTGC ACAACGGGTG
 3001 CTGCGGATGG GCGACGACGA ACGCCTTGGT GTAGCCGAGC ACGCACTGGT
 3051 TGAAGCGGGGA GATCT

Fig. 25B

119/133

PhnA protein SEQ ID NO:130

1 MGARRWLVS G VGYRLEESLE YRTLVP EALS IWRMAGANRM LFDCFDVDSK
51 AARRSVAILS SCLRIECWGR DVVLRALNSN GRALLAPLSE DCPAQVTCLR
101 DGDTLHWRF P QEE SHADEWR RLHGLSSLEA LRRVLGTLGD AEGPVLLGGL
151 FSFDLAEQFE PLPAPAE PAR HCPDYLFLVP ELLLDIDHLA RRTSLQAFVH
201 DPAGHDRLA A SLRQCADEFH GAVEEASESP VAGVRAGNYQ VDLDDASFAR
251 QVERLQAHVR AGDVFQIVPS RSFSMP CADD WRAYRQLCLR NPSPYRFFLD
301 AGDFCLFGAS PESALKYDAE SREVELYPIA GTRPRGRDAR GAIDAE LDNR
351 LEAE LRLDAK EIAEHMLVD LARNDLARVC RSGTRQVRDM LKVD RYSHVM
401 HLVSRVAGEL HGEL DALHAY RACLN MGT LV GAPKVRAMQL LRQYEDGYRG
451 SYGGAIGILD SAGN LDT SIV IRS AEVREGI ARV RAGAGVV LDSDP RLEAE
501 ETRNKALAVL TAVAAERER GERDAHHAVG

Fig. 26

PA14 degP SEQ ID NO:131

1 CGTCCGATT C GGCCTGAGTC TTTCTCTTCC CTCGAACATC ACGGGAGCTG TAGTCGATGC
61 ATACCCTAAA ACGCTGTATG GCTGCGATGG TGGCCTTGCT GGCCTTGAGC CTGGCGATGA
121 CGGCCCGGGC AGAACTGCCG GACTTCACGC CTTGGTCGA ACAGGCGTCG CCGGCGGTGG
181 TGAATATCAG TACGCCGCAG AAGCTGCCGG ATCCGCATGCCAT GGCGCGCGGG CAGCTGTCCA
241 TCCCCGACCT CGAAGGGCTG CCGCCGATGT TCCGCGACTT CCTCGAGCGC ACGATCCCGC
301 AGGTTCCGCG CAATCCGC CGGGCAGCAGC GCGAGGCGCA ATCGCTGGGC TCCGGCTTCA
361 TCATCTCCAA CGACGGCTAC ATCCTCACCA ACAATCACGT CGTGGCCGAT GCCGACGAGA
421 TCCCTGGTGC CGTCCGAC CGTAGCGAGC ACAAGGCCAA GCTGGTCCGGC GCGGACCCCGC
481 GCAGCGACGT GGCGGTGTG AAGATCGAGG CGAAGAACCT GCCGACCCCTG AACTGGCG
541 ATTGAAACAA GCTGAAAGTG GGCAGATGGG TCCCTGGCCAT CGGTTCGCCG TTCGGCTTCG
601 ATCACTCGGT CACCGCCGGT ATCGTCAGTG CCAAGGGCG TAGCCTGCCG AACGAGAGCT
661 ACGTACCCCTT CATCCAGACC GACGTGGCGA TCAACCCGGG CAACTCCGGC GGTCCGCTGC
721 TGAACCTGGA GGGCGAAGTG GTCCGGCATCA ACTCGCAGAT CTTCACCCGT TCCGGCGGT
781 TCATGGGCCT GTCCCTCGCC ATCCCGATCG ATGTCGCGCT GAACTCGCC GACCAGTTGA
841 AGAAAGCCGG CAAGGTCAGC CGCGGCTGGC TGGGTGTGGT GATCCAGGAA GTGAACAAGG
901 ATCTCGCCGA GTCCCTCGGC CTCGACAAGC CGTCCGGCGC GCTGGTGGCG CAGCTGGTGG
961 AAGACGGTCC GGC GGCGCAAG GGC GGCGCTGC AGGTGGGCGA TGTGATCCTC AGCCTGAACG
1021 GCCAGTCGAT CAACGAGTCC GCGGACCTGC CGCACCTGGT GGGCAACATG AAGCCGGCG
1081 ACAAGATCAA CCTGGACGTG ATTGCAACG GCCAGCGCAA GTCCCTTGAGC ATGGCGGTAG
1141 GCAACCTTCC GGACGACGAC GAGGAATCG CCTCGATGGG CGCTCCGGGC GCCGAGCGCA
1201 GCAGCAACCG CCTGGGCGTG ACCGTCGCCG ACCTGACCGC CGAGCAGCGC AAGAGCCTGG
1261 ATATCCAGGG CGGCGTGGTG ATCAAGGAAG TCCAGGACGG TCCGGCCGCG GTCATCGGCC
1321 TGC GTCCGGG CGATGTCATC ACCCACCTGG ACAACAAGGC GGTGACCTCG ACCAAGATCT
1381 TCGCCGACGT GGCC AAGGCC CTGCCGAAGA ACCGTTCGGT TTCGATGCCG GTACTG

Fig. 27

120/133

PA14 degP protein SEQ ID NO: 132

1 MHTLKRCMAA MVALLALSLA MTARAELPDF TPLVEQASPA VVNISTRQKL
51 PDRAMARGQL SIPDLEGLPP MFRDFLERTI PQVPRNPRGQ QREAQSLGSG
101 FIISNDGYIL TNNHVVADAD EILVRLSDRS EHAKAKLVGAD PRSDAVLKI
151 EAKNLPTLKL GDSNKLKVGE WVLALIGSPFG FDHSVTAGIV SAKGRSLPNE
201 SYVPFIQTDV AINPGNSGGP LLNLEGEVVG INSQIFTRSG GFMGLSFAIP
251 IDVALNVADQ LKKAGKVSRG WLGVVIQEVN KDLAESFGLD KPSGALVAQL
301 VEDGPAAKGG LQVGDVILSL NGQSINESAD LPHLVGNMKP GDKINLDVIR
351 NGQRKSLSMSA VGNLPDDDEE IASMGAPGAE RSSNRLGVTV ADLTAEQRKS
401 LDIQGGVVIK EVQDGPAAVI GLRPGDVITH LDNKAVTSTK IFADVAKALP
451 KNRSVSMRVL

Fig. 28

PA 8830 algD SEQ ID NO:133

1 GCGCGACAAA CAATCGAGGT GAATGCGATG CGAACATCAGCA TCTTTGGTTT
51 GGGCTATGTC GGTGCGAGTAT GTGCTGGCTG CCTGTCGGCA CGCGGTCACTG
101 AAGTCATTGG TGTGGATGTC TCCAGCACCA AGATCGACCT GATCAACCAG
151 GGCAAGTCGC CCATCGTCGA ACCGGGCCTG GAAGCGTTGT TGCAGCAAGG
201 CCGGCAGAACCG GAGACGGCTGT CGGGCACCCAC CGACTTCAAG AAGGCTGTGC
251 TGGACTCCGA CGTATCGTTC ATCTGCGTCG GCACGCCGAG CAAGAAGAAC
301 GGGCACCTGG ACCTGGGCTA CATCGAGACC GTCTGCCCG AGATCGGCTT
351 CGCCATCCGC GAGAAAGTCG AAGGCCACAC CGTGGTGGTG CGCAGCACCG
401 TACTGCCGGG CACCGTCAAC AACGTGGTGA TCCCGCTGAT CGAGGACTGC
451 TCGGGCAAGA AGGCCGGGGT CGACTTCGGC GTCCGGCACCA ACCCCGAATT
501 CCTCCCGCAG AGCACCGCGA TCAAGGACTA CGACTTCCCG CCGATGACCG
551 TGATCGGCCGA ACTGGACAAG CAGACGGCG ACCTTCTCGA GGAAATCTAC
601 CGCGAGCTGG ACGCGCCGAT CATCCGCAAG ACCGTCGAGG TCGCCGAGAT
651 GATCAAGTAC ACCTGCAACG TCTGGCACGC CGCCAAGGTC ACCTTCGCCA
701 ACGAGATCGG CAACATCGCC AAGGGCGTCG GCGTCGACGG CGCGAGGTG
751 ATGGACGTGA TCTGCCAGGA CCACAAGCTC AACCTGTCGC GCTACTACAT
801 GCGTCCCGC TTGCGCTTCG GCGGCTCCTG CCTGCCCAAG GATGTACGCG
851 CCCTCACCTA TCGCGCCAGC CAGCTGGACG TCGAGCACCC GATGCTCGGT
901 TCGTTGATGC GCAGCAACTC CAACCAGGTG CAGAAGGCCT TCGATCTCAT
951 CACCAGCCAC GACACCCGCA AGGTGGCCT GCTCGGCCCTG TCGTTCAAGG
1001 CCGGCACCGA CGATTGCGC GAAAGCCGC TGGTGGAGCT GGCGAGATG
1051 CTCATCGGCCA AGGGCTACGA GTTCCGCATC TTGACCGCA ACGTCAATA
1101 CGCGCGTGTGTC CACGGGGCCA ACAAGGAATA CATCGAGTCG AAGATCCCGC
1151 ACGTCTCCTC GCTGCTGGTC TCCGACCTCG AGGAAGTGGT GGCGAGTTCC
1201 GATGTGCTGG TGCTGGCAA TGGCGACGAG CTGTTCGTCG ACCTGGTGAA
1251 CAAGACCCCG AGCGGCAAGA AGCTGGTCGA CCTGGTGGGC TTCATGCCGC
1301 ACACCACCA TGCCAGGCC GAGGGCATCT GCTGGTAGCG G

Fig. 29

PA 8830 algD protein SEQ ID NO: 134

1 MRISIFGLGY VGAVCAGCLS ARGHEVIGVD VSSTKIDLIN QGKSPIVEPG
51 LEALLQQGRQ TGRLSGTTDF KKAVALSDVS FICVGTPSKK NGDLDLGYIE
101 TVCREIGFAI REKSERHTVV VRSTVLPGTV NNVVIPLIED CSGKKAGVDF
151 GVGTNPEFLR ESTAIKYDF PPMTVIGELD KQTGDLLEEI YRELDAPIIR
201 KTVEVAEMIK YTCNVWHAAK VTFANEIGNI AKAVGVDGRE VMDVICQDHK
251 LNLSRYYMMP GFAGGGSCLP KDVRALTYRA SQLDVEHPML GSLMRNSNSQ
301 VQKAFDLITS HDTRKVGLLG LSFKAGTDDL RESPLVELAE MLIGKGYEFR
351 IFDRNVEYAR VHGANKEYIE SKIPHVSSLL VSDLDEVVAS SDVLVLGNGD
401 ELFVDLVNKT PSGKKLVDLV GFMPHTTAQ AEGICW

Fig. 30

121/133

>Contig1126 of Mutant 25A12 SEQ ID NO: 135

..AACACCGGACGCGCCCCGATCATGTGCGCTGAGCGCTACGCTACCGTCAA
 CGAAAAAAGGCCACCTCGGGGTGGCCTTTCGCGTTCTCGCACCGATCGCG
 CGGAATATCGCGGTTAACGCCTCTCCCCCGTGCACCTGCACCTGCGGCTGAGC
 CTCAGAACGAAAGTCCGGCGGTAGGCACGGTAGCGCGGGAACAGAACGTT
 GCCTCGATGGCGTCTGTTCACTACCTCGCTGGTATGCAGGGCCTTGCC
 CTCGGCCTGGGCTGCTTGGCCACGGCGACGGCGATGCACCTGCTGACCT
 CGCGGATGTCGCCAGCGCCGGCAACACGGCGCCCTGCCCTGGTAACG
 ATCGGGCAGCAGTGGCCAGGGCGTTGGCCGGCCATCAGCATGCCTTC
 GGTGACCCGATTGGCCCGCGCGCGATCACCCCCAGGCCGATGCCGGGA
 AGATATAGGCCTGTTGCACTGGCGATGGGAATCCGCTGTCGCCACC
 TGCACCGGTTGGAACGGGCTACCGGTGGCGACCAGCGCCTGGCGTGGT
 CCAGTTGAGGATTTCCTGCGGAGTCGCCTCGACCCCGAGGTCGGTTGG
 ACAGCGGCATCACCAAGCGGCTGCTGCAATGGCTGTGCAGCTACGGATG
 ACCTCTCGGAAAACAGCCCGCGCTGCCCGAGACGCCGATCAGCACCGT
 CGGCCGGGCGATTGCGGATCACTCCAGCAACGCCAGGTCGTGCCCTGCT
 GGCGCCCGAGGACCGAGATCGCGCGCTCTGCGCCAGGCGGTGCTGG
 AAGTCGACCAGGTTGCTCATGTCGTCGGTGAGCAGGCCAGCGGTGAC
 CATGAAGATGCGCCGACGCCCTGGCCTCGTCCAGGCCCTCCAGTTGCA
 TGGCGCGATGATCTGTTGGCGATGCCGAACCCGGGAGGGGCGCCGA
 CGAAGGTACGGCTGCTCGTCACTCGCCCTGGCCTTGCAAGCC
 GCCAGCAGGGTGCCACGCCACCGCGCGTGCCCTGGATGTCGTGCTT
 GAAGCAGCACAGCTGCTCTGCAATTGCAAGCAGGACGTTGGCCAGCGCGCTTG
 ATCGCCTGGATGAACAGGTGCAAGAACCTCGTACTGCCCGCTCAC
 CCGCTCGTGGCGCCACCAATGTACATCGGGTCGTTGAGCAGGTCCGGT
 TGTTGGTGCCGACGTCCAGCACCCACGGCAGGGTGTAGGCCGGCTGATA
 CCGCCGAGGTGTAACAGGGACAGCTGCCGATGGGATGCCCATCCGG
 CCGATGCCCTGGTGCCGAGGGCGAGGATCGGCTGGCTGTCGGTACAAAA
 CAATCTAAGGTGCTTGGCTGAAAGGAGTTCAATCGTTGGCCGGCG
 GGAAGAATAAAGGCCGGTGGCTGAAACTTGAATCTGGAAGGTTGCAA
 ACTGGGGGAAAAATGAAATTAAAGAGCCTAACAGAGCGAAAAAGTT
 CTTTTCTAAAAGAAAAATGGGAAAAGTTGAAAGGCCAGTGAATAACTCTGG
 GAGCAGGTGTCAAATGAATGTTGAAAGGCCAGTGAATAACTCTGG
 AAAAGGCAGTTATAAGGGCTATAAAAGGGATGAAAAAGAAGTGTGTGAA
 ATAACGAAAGGCAATAGGGAAA

Fig. 31

33C7 contig Map (1 > 2048) ORF Map

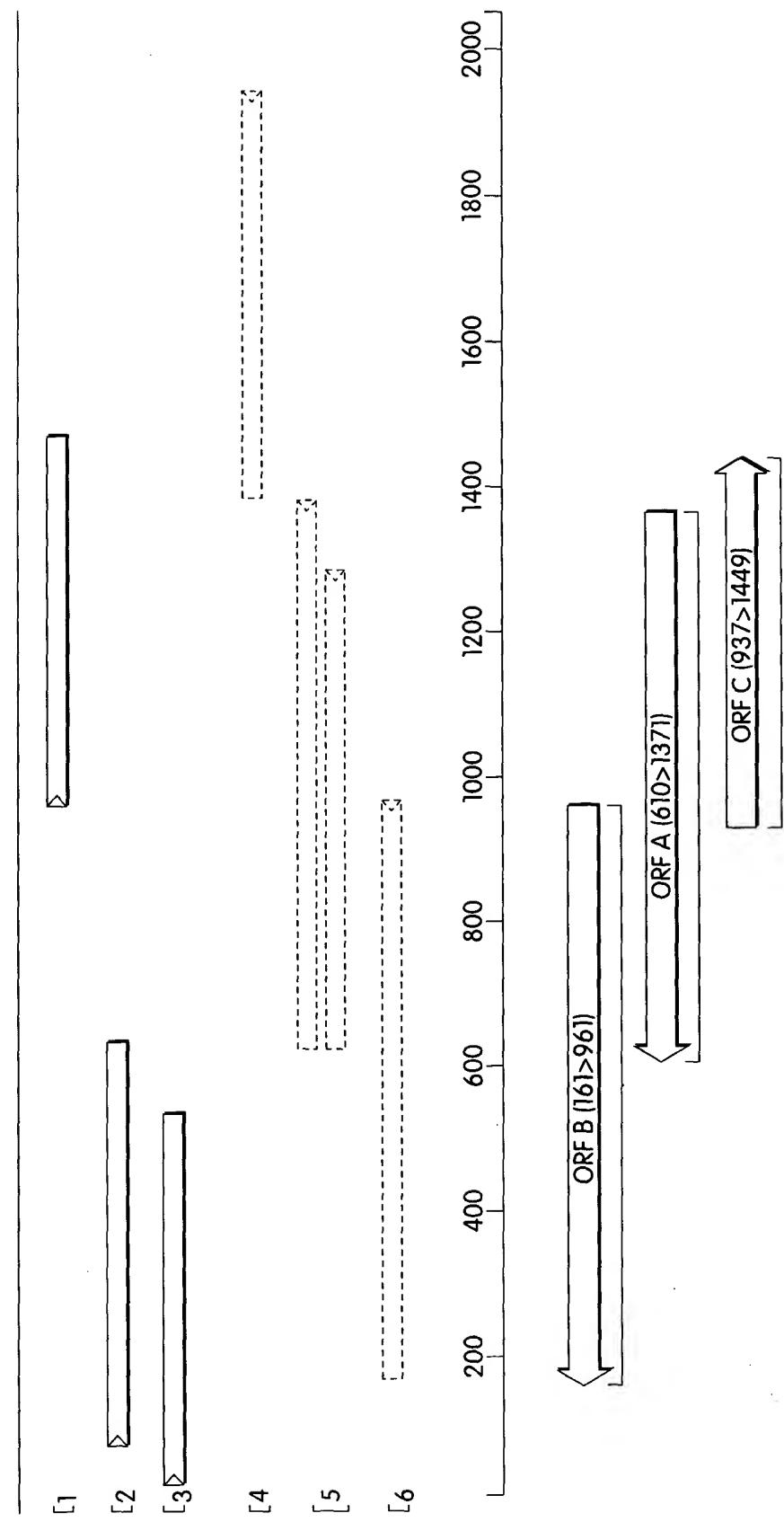


Fig. 32A

124/133

Sequence: 33C7 contig From: 1 To: 2048

10 20 30 40 50 60
120 180 240 300
310 320 330 340 350 360
360 420 480 540 600
610 620 630 640 650 660
660 720 780 840 900
910 920 930 940 950 960
960 1020 1080 1140 1200
1210 1220 1230 1240 1250 1260
1260 1320 1380 1440 1500

AGCTTATGCA TGCGGCCGCA TCTAGAGGGC CCGGATCCGG TGACCATCGG TCACCGGCAT 60
GCCGGTGGTT TCGGTATCCA GTACGACGCT ACGCATCTAT AGAGCCTTTC TCTGTTTGC 120
TGCAGCCGTG GCTGCTGAAC GCTTGTTCG GTGTGGCCGC TCAGCCGGC AATTCCGGCA 180
CGCCACGGTT GGCAACTGG TCGGCCGCT CGTTGCCGGG GTGCCGGTA TGCCCGCGGA 240
CCCACTGCCA CTCCACCTGG TGCCGGCGA CCTGTTCATC CAGGGCCTGC CAGAGGTGG 300
CATTCTTGAC AGGCTGCTTG CTGGCGGTCT TCCAGCCGCG CTTCTTCAG TTCGGCAACC 360
ATTCCGGTGT GCGCGGCATC ACGTATTCCG AGTCGGTGT CAGACGGATC GGACAGGAAC 420
GCTTGAGTGC CGCCAGCGCC TGGATCGCCG CCATCAGCTC CATGCGGTG TTGGTGGTGT 480
CCGGCTCGCC GCCCCAAAGC TCTCGCTCGG CGCCCTTGTA GAGGAGCAAC GCCCCCCAGC 540
CGCCGCGCCC AGGGTTGCCG TTGCAGGCGC CGTCGGTATA GATCACTACC TGTTCTTTAT 600
CTGTCATGCC TAAATTCGG AATCTGCCG GCTGACTTTG GCCACCGGCA TGGGCACCAAG 660
CTGACCGGCC GGTTCGGCCT TGCTCTGGCG CAAACGGGCGC AACCCCCACGA CCAGCTTGCG 720
TGCCACCAAT AGATAGAACG CGGCGCCCGA AGACTGCCAG GCGTCCGCCCC AGCGCTCCAG 780
GCGAGGCCAGG CGCGATTGCC AGGCTGCCGA CGCAAGCGGC GGACGATAGC ACCCGAAGGC 840
CCGTTTCTCC AGCGCGAACG CCAGCAGGTT GAGCCAATCG CAGGCCCGCG ACGGAGGAAT 900
GCAGCGGGCC TGGCGCAAGG CATCCCCGGC GAAATAATGA CGGATGCCCG ACAGGCTCCA 960
TGGGTTGATG CCGATCAGCA GCAGGGTGGCC GCCCGGACGA ACGGTACGCG CGGCTTGCG 1020
CAGGAGACGG TGAGGCGACA GGCAGAAATC CAGGCCGTGT TGCAGCAGGA CCACGTCCGC 1080
GGCATGTTCG CTGAGCGGCC AGGCGCCCTC TTGCGAGGCG ATGTCCACGC CGGGCAGCGG 1140
CGGCCCCAGG CGCACGCCGC GCTGAATCTG CCCGGTGCTC GGCGCAGTT CGGCATGCGG 1200
CCCGTAGTGC ACCAGGTAGC CACCGAAGTA ACGGGTCAGC TCGTCGCACA ACAGGCGTCG 1260
CTCCTCGGCC AGCATCAGGC TGCCCCAGCGG GCCCTGGAAC CAGTCGGCGC CCCGGTTGAT 1320
CGATGCCAGC CACTCGGCAT CGGTCTGGGC GAAGGCTTGC GGTTCGTTCA TGCCTACCTC 1380
CAGCGTCTTC CCCTTCGCGG CGACGGACGC CGGCACGACG GGAAAATAAG CAATACTATG 1440
CGCCAATGAC TTCTGCTTAG CGACATCGAC CCATGATACA GATCGACGCC CTGCCCGCCT 1500

Fig. 32B

125/133

Sequence: 33C7 contig From: 1 To: 2048 (continued)

1510 1520 1530 1540 1550 1560
TCAACGACAA CTACATCTGG CTGTTGCAAG ATGCGACAAG CCGTCGCTGC GCGGTGGTCG 1560
ACCCCAGCGA TGCCAAGCCG GTGGAAGCCT GGCTGGCCGC CCATCCCGAC TGGCGGTTGA 1620
GCGATATCCT GGTGACCCAC CACCATCACG ACCACGTCGG CGGCGTCGCG GCCCTGAAGG 1680
AACTGACCGG CGCGCGGGTT CTCGGCCCGG CCAACGAGAA GATCCCGGCC CGCGACCTGG 1740
CGCTGGAAGA CGCGAACCGG GTCGAGGTGC TCGGCCTGGT CTTCGAGATC TTCCACGTGC 1800
1810 1820 1830 1840 1850 1860
CCGGCCATAC CCTCGGCCAT ATCGCTACT ACCACCCGGC GGAGACGCCG CTGCTGTTCT 1860
GCGGCGACAC CCTGTTCGCC GCCGGCTGCG GCCGTCTCTT CGAAGGCACC CGGGCGCAGA 1920
TGCACCATTC CCTGGCGCGA CTGGCCGCGC TGCCGGCAA CACCCGGTC TACTGCACCC 1980
ACGAGTACAC GCTGAGAAC CTGCGCTTCG CGCTGGCGGT GGAGCCCGAC AACGCGCGC 2040
TGCAGGAA 2048

Fig. 32C

33C7 ORF A

ATGAACGAAC CGCAAGCCTT CGCCCAGACC GATGCCGAGT 40
GGCTGGCATC GATCAACCAGG GCGCGCGACT GGTTCCAGGG 80
CCCGCTGGGC AGCCTGATGC TGGCCGAGGA GCGACGCTG 120
TTGTGCGACG AGCTGACCCG TTACTTCGGT GGCTACCTGG 160
TGCACTACGG GCCGCATGCC GAACTGCCGC CGAGCACCGG 200

GCAGATTCA CGCGGCGTGC GCCTGGGGCC GCCGCTGCCG 240
GGCGTGGACA TCGCCTGCGA AGAGGGCGCC TGGCCGCTCA 280
GCGAACATGC CGCGGACGTG GTCCTGCTGC AACACGGCCT 320
GGATTTCTGC CTGTCGCCTC ACCGTCTCCT GCGCGAAGCC 360
CGCGTACCG TTCGTCCGGG CGGCCACCTG CTGCTGATCG 400

GCATCAACCC ATGGAGCCTG TGGGGCATCC GTCATTATTT 440
CGCCGGGGAT GCCTTGCGCC AGGCCCGCTG CATTCTCCG 480
TCGCGGGCCT GCGATTGGCT CAACCTGCTG GGCTTCGCGC 520
TGGAGAAACG GCGCTTCGGG TGCTATCGTC CGCCGCTG 560
GTCGGCAGCC TGGCAATCGC GCCTGGCTCG CCTGGAGCGC 600

TGGGGCGACG CCTGGCAGTC TTCGGCGGCC GGCTTCTATC 640
TATTGGTGGC ACGCAAGCTG GTCGTGGGGT TGCGCCCGTT 680
GCGCCAGAGC AAGCGCGAAC CGCGCGGTCA GCTGGTGCCC 720
ATGCCGGTGG CGAAAGTCAG CGGGCGAGAT TCCGAAATTT 760
AG 762

Fig. 32D

126/133

Sequence: 33C7 ORF A From: 1 To: 254

10 20 30 40
MNEPQAFQQT DAEWLASINR ARDWFQGPLG SLMLAEERRL 40
LCDELTRYFG GYLVHYGPHA ELPPSTGQIQ RGVRLGPPLP 80
GVDIACEEGA WPLSEHAADV VLLQHGLDFC LSPHRLLREA 120
ARTVRPGGHL LLIGINPWSL WGIRHYFAGD ALRQARCIIPP 160
SRACDWLNLL GFALEKRRFG CYRPPLASAA WQSRLARLER 200
WGDAWQSSGA GFYLLVARKL VVGLRPLRQS KREPRGQLVP 240
MPVAKVSRRD SEI. 254

Fig. 32E

Sequence: 33C7 ORF B From: 1 To: 801

10 20 30 40 50 60
ATGGAGCCTG TGGGGCATCC GTCATTATTT CGCCGGGGAT GCCTGCGCC AGGCCCCTG 60
CATTCCCTCCG TCGCGGGCCT GCGATTGGCT CAACCTGCTG GGCTCGCGC TGGAGAACG 120
GCGCTTCGGG TGCTATCGTC CGCCGCTTGC GTCGGCAGCC TGGCAATCGC GCCTGGCTG 180
CCTGGAGCGC TGGGGCAGC CCTGGCAGTC TTCGGGCGCC GGCTTCTATC TATTGGTGGC 240
ACGCAAGCTG GTCGTGGGGT TGCGCCCGTT GCGCCAGAGC AAGCGCGAAC CGCGCGGTCA 300
310 320 330 340 350 360
GCTGGTGCCTC ATGCCGGTGG CGAAAGTCAG CCGGGCAGAT TCCGAAATT AGGCATGACA 360
GATAAAAGAAC AGGTAGTGAT CTATACCGAC GGCGCCTGCA AGGGCAACCC TGGGCGCGGC 420
GGCTGGGGGG CGTTGCTCCT CTACAAGGGC GCGGAGCGAG AGCTTGGGG CGGCGAGCCG 480
GACACCACCA ACAACCGCAT GGAGCTGATG GCGGCGATCC AGGGCCTGGC GGCACCTCAAG 540
CGTTCTGTC CGATCCGTCT GATCACCGAC TCGGAATAACG TGATGCGCGG CATCACCGAA 600
610 620 630 640 650 660
TGGTTGCCGA ACTTGGAAAGAA GCGCGGCTGG AAGACCGCCA GCAAGCAGCC TGTCAAGAAT 660
GCCGACCTCT GGCAGGCCCT GGATGAACAG GTCGCCCGGC ACCAGGTGGA GTGGCAGTGG 720
GTCCGCGGGC ATACCGGCGA CCCCGGCAAC GAGCGGGCCG ACCAGTTGGC CAACCGTGGC 780
GTCGCCGAAT TGCCGCGCTG A 801

Fig. 32F

Sequence: 33C7 ORF B PROTEIN From: 1 To: 267

10 20 30 40 50
MEPVGHPSLF RRGCLAPGPL HSSVAGLRLA QPAGLRAGET ALRVLSSAAC 50
VGSLAIAPGS PGALGRRLLAV FGRRLLSIGG TQAGRGVAPV APEQARTARS 100
AGAHAGGESQ PARFRNLGMLT DKEQVVIYTD GACKGNPGRG GWGALLLYKG 150
AERELWGGEPE DTTNNRMELM AAIQALAALK RSCPIRLITD SEYVMRGITE 200
WLPNWKKRGW KTASKQPVKN ADLWQALDEQ VARHQVEWQW VRGHTGDPGN 250
260 270 280 290 300
ERADQLANRG VAEPLPR. 267

Fig. 32G

127/133

33C7 ORF C

10 20 30 40 50 60
ATGACGGATG CCCCACAGGC TCCATGGGTT GATGCCGATC AGCAGCAGGT GGCCGCCCGG 60
ACGAACGGTA CGCGCGGCTT CGCGCAGGAG ACGGTGAGGC GACAGGCAGA AATCCAGGCC 120
GTGTTGCAGC AGGACCACGT CCGCGGCATG TTCGCTGAGC GGCCAGGCCGC CCTCTTCGCA 180
GGCGATGTCC ACGCCCGGCA GCGGCGGCC CAGGCGCACG CCGCGCTGAA TCTGCCCGGT 240
GCTCGGCGGC AGTTCGGCAT GCGGCCCGTA GTGCACCAAGG TAGCCACCGA AGTAACGGGT 300
310 320 330 340 350 360
CAGCTCGTCG CACAACAGGC GTCGCTCCTC GGCCAGCATC AGGCTGCCCA GCAGGGCCCTG 360
GAACCAGTCG CGCGCCCGGT TGATCGATGC CAGCCACTCG GCATCGGTCT GGGCGAAGGC 420
TTGCGGTTCG TTCATGCGTA CCTCCAGCGT CTTCCCCCTTC GCGGCGACGG ACGCCGGCAC 480
GACGGGAAAA TAAGCAATAC TATGCGCCAA TGA 513

Fig. 32H

Sequence: 33C7 ORF C PROTEIN From: 1 To: 171

10 20 30 40 50
MTDAPQAPWV DADQQQVAAR TNGTRGFAQE TVRRQAEIQA VLQQDHVRGM 50
FAERPGALFA GDVHARQRRP QAHAAALNLPG ARRQFGMRPV VHQVATEVTG 100
QLVAQQASLL GQHQAAQRAL EPVARPVDRQ QPLGIGLGEGLR FVHAYLQR 150
LPLRGDGRRH DGKISNTMRQ . 171

Fig. 32I

1G2 SEQ ID NO:137

1 NTTGTGTTAA GATCAGGCTT GGTGGTGAAG AAAGGTTCGA ACNNGTGGTC
51 AATGATCNAC TTCGGGGATN CNGCTGCCG TATNATTCAA CACGTGGTCA
101 AACGGTATGT TCCGAGGCCT CTGNCCACCN GTACTAGTCG ACGC

Fig. 33

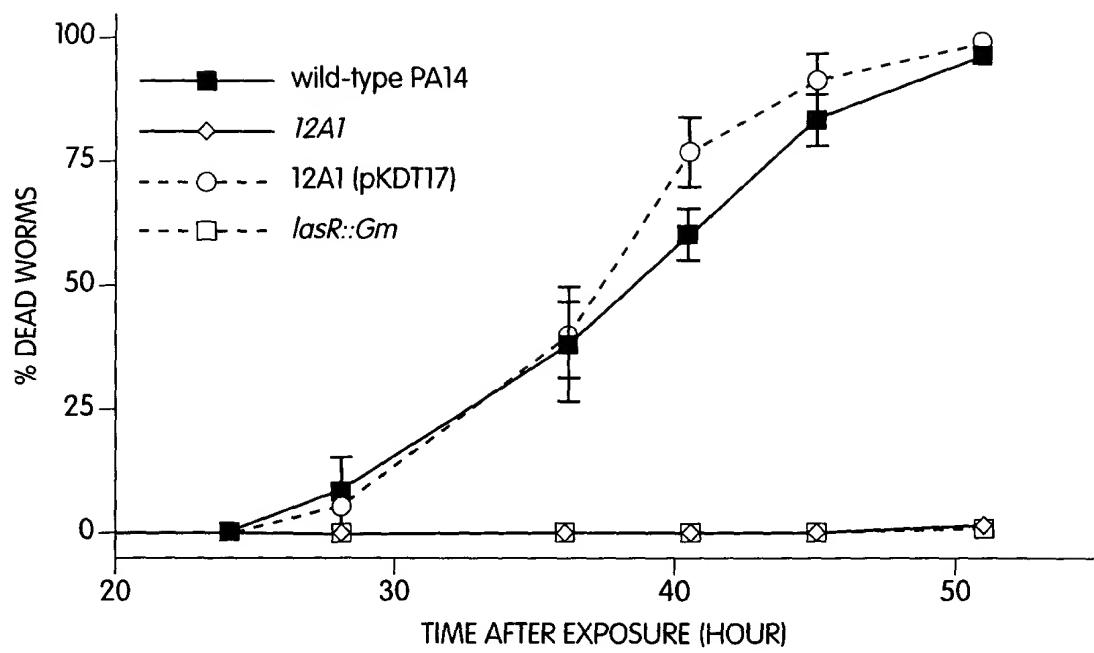


Fig. 34A

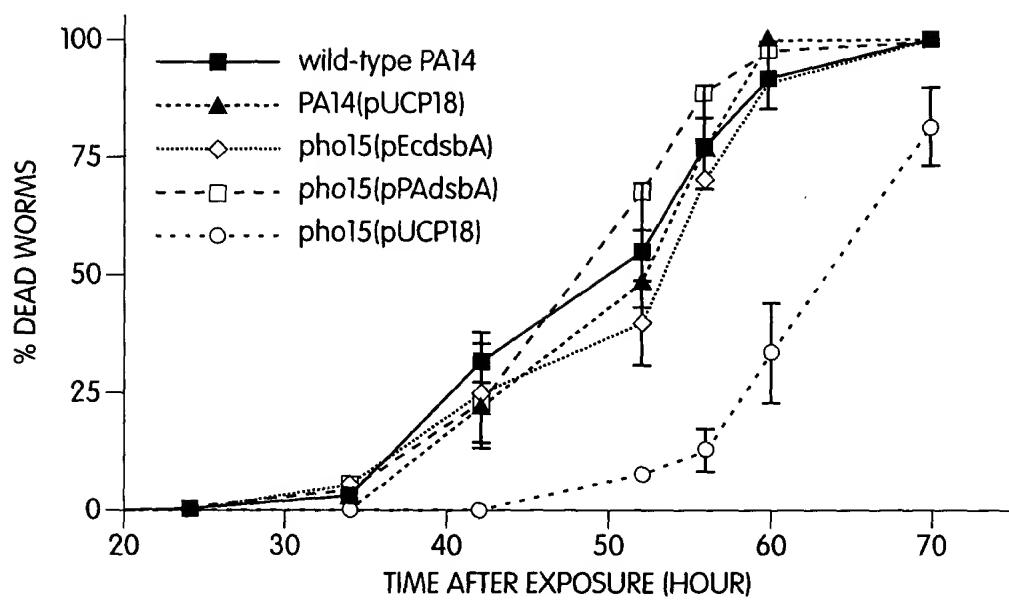


Fig. 34B

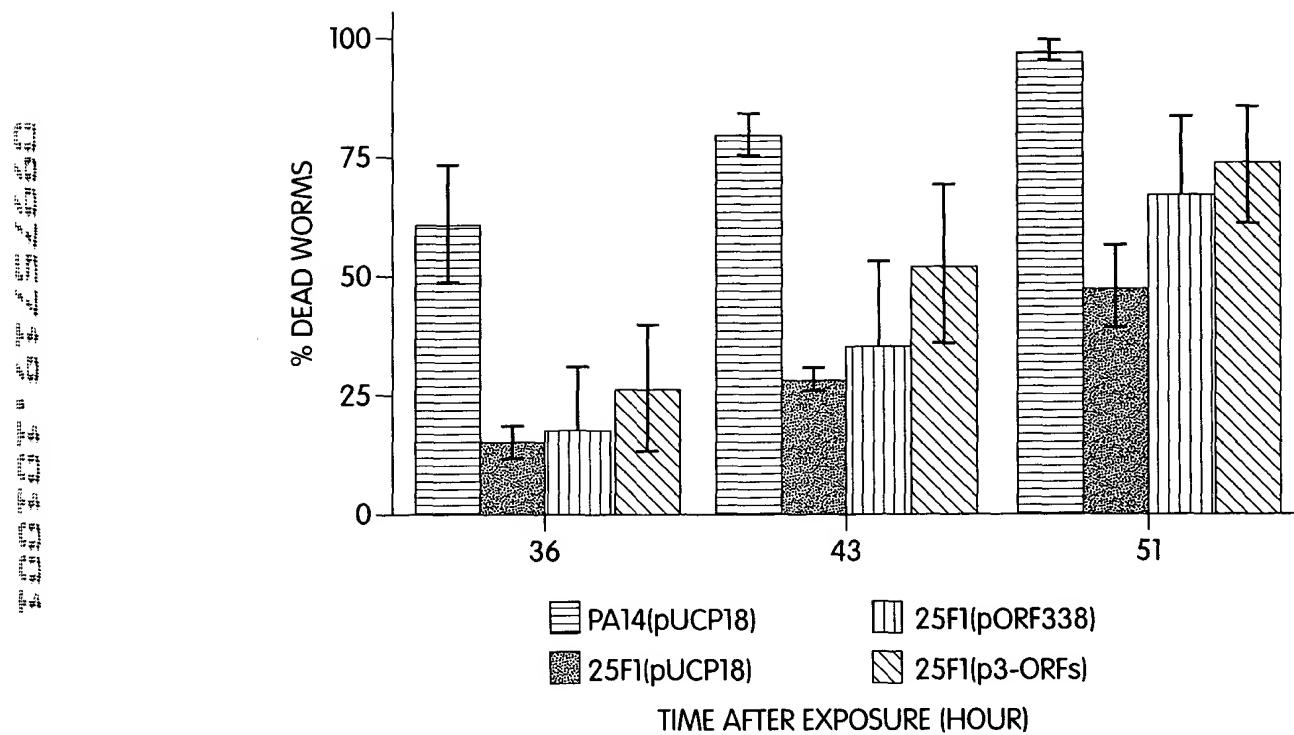


Fig. 34C

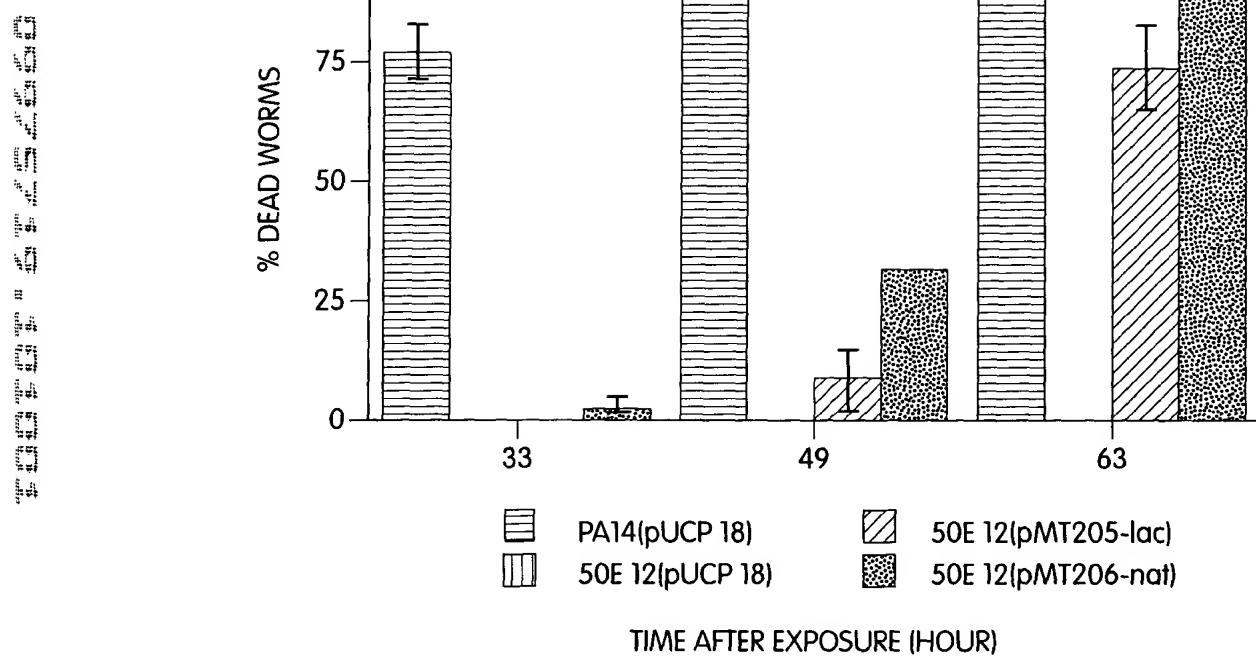


Fig. 34D

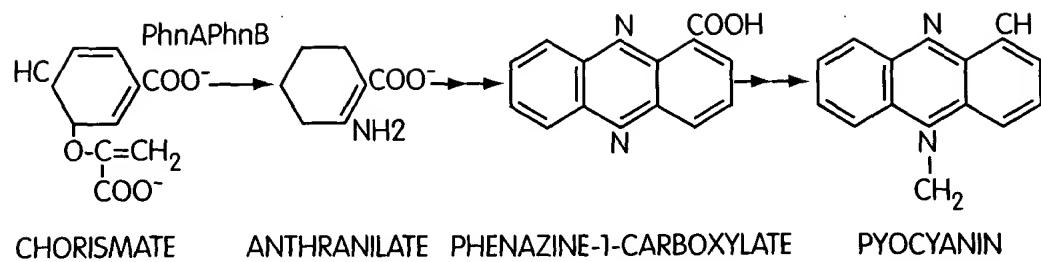


Fig. 35A

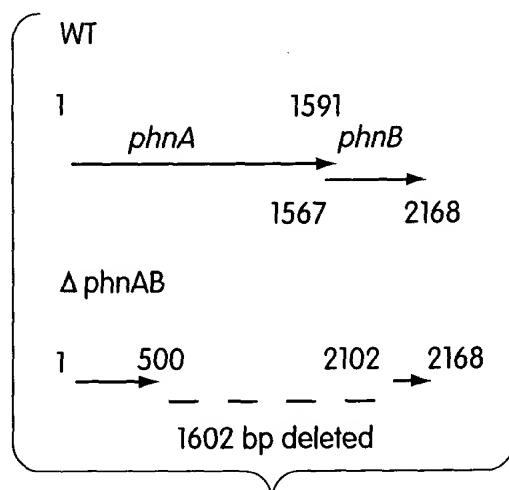


Fig. 35B

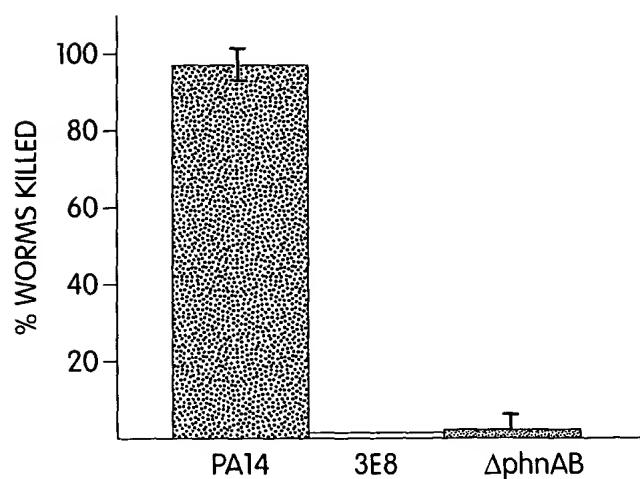


Fig. 35C